

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:05:16 ; Search time 36 Seconds

(without alignments)
655.149 Million cell updates/sec

Title: US-10-000-157-6

Sequence: 1 MREPRLEGDSLSLFLQV.....ERRLYRVSLACVCPRVWG 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

```
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	985	100.0	177 22 AAU04952	Human Interleukin PRO10272
2	985	100.0	177 22 AAB47299	Human Interleukin PRO10272
3	985	100.0	177 22 AAB87603	Human Interleukin PRO10272
4	985	100.0	177 22 AAB07598	Human Interleukin PRO10272
5	898	91.2	161 21 AAB07692	Human Interleukin PRO10272
6	898	91.2	161 21 AAE18120	Human Interleukin PRO10272
7	898	91.2	161 23 AAM52691	Human Interleukin PRO10272
8	898	91.2	161 23 AAM47464	Human Interleukin PRO10272
9	834	84.7	350 22 ABG29372	Human Interleukin PRO10272
10	697	70.8	169 21 AAB07600	Human Interleukin PRO10272

11	697	70.8	169 21 AAB07694	Human Interleukin PRO10272
12	697	70.8	169 23 AAE18121	Human Interleukin PRO10272
13	697	70.8	169 23 AAM52692	Human Interleukin PRO10272
14	670	68.0	160 23 AAE18122	Human Interleukin PRO10272
15	351.5	35.7	144 21 AAB07599	Human Interleukin PRO10272
16	351.5	35.7	144 21 AAB07693	Human Interleukin PRO10272
17	170.5	17.3	206 21 AAY44185	Human Interleukin PRO10272
18	165.5	16.8	187 21 AAE23794	Human Interleukin PRO10272
19	165.5	16.8	197 21 AAB18911	Human Interleukin PRO10272
20	165.5	16.8	197 21 AAB07602	Human Interleukin PRO10272
21	165.5	16.8	197 21 AAB07684	Human Interleukin PRO10272
22	165.5	16.8	197 21 AAY92238	Human Interleukin PRO10272
23	165.5	16.8	197 21 AAY44460	Human Interleukin PRO10272
24	165.5	16.8	197 21 AAY53892	Human Interleukin PRO10272
25	165.5	16.8	197 22 AAG66121	Human Interleukin PRO10272
26	165.5	16.8	197 22 AAU29247	Human Interleukin PRO10272
27	165.5	16.8	197 22 AAU04951	Human Interleukin PRO10272
28	165.5	16.8	197 23 AAU23792	Human Interleukin PRO10272
29	165.5	16.8	227 22 AAE08676	Human Interleukin PRO10272
30	165.5	16.8	227 22 AAE08679	Human Interleukin PRO10272
31	165.5	16.8	227 22 AAE08680	Human Interleukin PRO10272
32	165.5	16.8	227 22 AAE08681	Human Interleukin PRO10272
33	165.5	16.8	227 22 AAE08682	Human Interleukin PRO10272
34	165.5	16.8	227 22 AAE08683	Human Interleukin PRO10272
35	165.5	16.8	227 22 AAE08684	Human Interleukin PRO10272
36	165.5	16.8	425 21 AAY44462	Human Interleukin PRO10272
37	165	16.8	223 22 AAE08677	Human Interleukin PRO10272
38	163.5	16.6	227 22 AAE08685	Human Interleukin PRO10272
39	161.5	16.4	227 22 AAE08687	Human Interleukin PRO10272
40	160.5	16.3	227 22 AAE08686	Human Interleukin PRO10272
41	157.5	16.0	227 22 AAE08690	Human Interleukin PRO10272
42	156.5	15.9	227 22 AAE08688	Human Interleukin PRO10272
43	156.5	15.9	227 22 AAE08689	Human Interleukin PRO10272
44	156.5	15.9	227 22 AAE08691	Human Interleukin PRO10272
45	156.5	15.9	227 22 AAE08693	Human Interleukin PRO10272

ALIGNMENTS

RESULT 1	AAU04952	standard; Protein: 177 AA.
ID	AAU04952	
XX	AAU04952	
AC	24-OCT-2001	(first entry)
XX		
DT	Human Interleukin 17E ligand, IL-17E.	
XX		
DE	Human Interleukin 17E ligand, IL-17E.	
XX		
KW	Human; Interleukin-17E ligand; IL-17E; agonist; antagonist; PRO10272; DNA 147531-2821; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus; allergic disease; asthma; demyelinating disease; degenerative cartilaginous disorder; transplantation associated disease.	
KW		
XX		
OS	Homo sapiens.	
XX		
FX		
FT	Key	Location/Qualifiers
FT	Reptide	1..32
FT	Protein	/label= Signal-peptide
FT	Region	33..177
FT	Region	/label= Mature_IL_17E
FT	Region	44..50
FT	Region	/note= "N-myristoylation site"
FT	Region	127..135
FT	Region	/note= "Tyrosine kinase phosphorylation site"
FT	Region	136..140
FT	Region	/note= "Asn is glycosylated"
FT	Region	150y..156
FT	Region	/note= "N-myristoylation site"
XX		
PN	WO200146420-A2.	

XX 28-JUN-2001.
 XX 20-DEC-2000; 2000MO-US34956.
 XX 23-DEC-1999; 99US-0172096.
 XX 30-DEC-1999; 99MO-US31274.
 XX 11-JAN-2000; 2000US-0175481.
 XX 18-FEB-2000; 2000MO-US04341.
 XX 02-MAR-2000; 2000MO-US05841.
 XX 21-MAR-2000; 2000MO-US01007.
 XX 21-MAR-2000; 2000MO-US07532.
 XX 02-JUN-2000; 2000MO-US15264.
 XX 22-JUN-2000; 2000US-0213087.
 XX 22-AUG-2000; 2000US-0644848.
 XX 24-AUG-2000; 2000MO-US23328.
 XX 24-OCT-2000; 2000US-0242837.
 XX 10-NOV-2000; 2000MO-US30873.
 XX 28-NOV-2000; 2000US-0253646.
 XX 01-DEC-2000; 2000MO-US32678.
 XX (GETH) GENENTECH INC.
 XX PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;
 XX PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;
 XX PI Watanabe CK, Williams PM, Wood WI, Yansura DG;
 XX MPI; 2001-451708/48.
 XX DR N-PSDB; AAS09511.
 XX PT Novel PRO polypeptides homologous to Interleukin-17, useful for the
 XX PT diagnosis and treatment of immune related disease e.g. rheumatoid
 XX PT arthritis and diabetes.
 XX Claim 10; Fig 6; 188pp; English.
 XX The sequence is PRO10272 which is the human Interleukin 17E ligand,
 XX IL-17E, encoded by DNA 147531-2821. A composition
 XX containing ant/agonists to the PRO polypeptides or individual components
 XX are useful for treating a mammal with an immune related disease, e.g.
 XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 XX thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
 XX disease, a demyelinating disease, an allergic disease or immune-mediated skin
 XX disease, contact dermatitis, an allergic disease e.g. food
 XX hypersensitivity, asthma, a transplantation associated disease, or a
 XX chronic inflammatory demyelinating polyneuropathy. Treating a PRO1031 or
 XX CC degenerative cartilaginous disorder comprises administering a PRO1031 or
 XX CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
 XX CC examples of the diseases and disorders are given in the specification.
 XX SQ Sequence 177 AA;
 XX
 XX Query Match 100.0%; Score 985; DB 22; Length 177;
 XX Best Local Similarity 100.0%; Pred. No. 2.6e-93;
 XX Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 MRRPRRLGSDSLISFLQYVAFAMVGTHTYSHWPSCCPSKQDTSSEELRMSTVFP 60
 XX DB 1 MRRPRRLGSDSLISFLQYVAFAMVGTHTYSHWPSCCPSKQDTSSEELRMSTVFP 60
 XX QY 61 PLPPARPNRHRESCRASEDPLNSRAISPMRYELDRDLNRLPOLYHARCCLCPHCVSLOT 120
 XX DB 61 PLPPARPNRHRESCRASEDPLNSRAISPMRYELDRDLNRLPOLYHARCCLCPHCVSLOT 120
 XX QY 121 GSHMDRGNSNELLHYNQTVFYRRPCHGEKGTHTKCYCLERLRYSLACVCPRPVWG 177
 XX DB 121 GSHMDRGNSNELLHYNQTVFYRRPCHGEKGTHTKCYCLERLRYSLACVCPRPVWG 177
 XX RESULT 2

AAB47299
 ID AAB47299 standard; Protein: 177 AA.
 XX AC AAB47299;
 XX 22-AUG-2001 (first entry)
 XX DE PRO10272 polypeptide.
 XX PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte;
 XX PRO1199; PRO1556; PRO4401; PRO10268; inhibition; stimulation;
 XX infiltration; mononuclear cell; eosinophili; erythema multiforme;
 XX polymorphonuclear neutrophil; PMN; antibody; immune-related disorder;
 XX systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 XX juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;
 XX idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease;
 XX systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; asthma;
 XX autoimmune thrombocytopaenia; thyroiditis; diabetes mellitus; allergy;
 XX immune-mediated renal disease; demyelination; central nervous system;
 XX peripheral nervous system; idiopathic demyelinating polyneuropathy;
 XX Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia;
 XX chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis;
 XX granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity;
 XX inflammatory bowel disease; gluten-sensitive enteropathy; urticaria;
 XX Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis;
 XX psoriasis; atopic dermatitis; hypersensitivity pneumonitis;
 XX graft rejection; graft-versus-host disease.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..32
 XX FT /label= Signal peptide
 XX FT Protein 33..177
 XX FT /label= Mature PRO10272
 XX FT Modified-site 44..50
 XX FT /label= N-myristoylation site
 XX FT Modified-site 127..135
 XX FT /label= Tyrosine kinase phosphorylation site
 XX FT Modified-site 136..140
 XX FT /label= N-glycosylation site
 XX FT Modified-site 150..156
 XX FT /label= N-myristoylation site
 XX PN WO200140465-A2.
 XX PD 07-JUN-2001.
 XX PF 10-NOV-2000; 2000MO-US30873.
 XX PR 30-NOV-1999; 99MO-US28313.
 XX PR 09-DEC-1999; 99US-0170262.
 XX PR 23-DEC-1999; 99US-0172059.
 XX PR 11-JAN-2000; 2000US-0175481.
 XX PR 20-JAN-2000; 2000US-0177118.
 XX PR 18-FEB-2000; 2000MO-US04342.
 XX PR 03-MAR-2000; 2000US-0187202.
 XX PR 30-MAY-2000; 2000MO-US14941.
 XX PR 05-JUN-2000; 2000US-0209832.
 XX PR 24-AUG-2000; 2000MO-US23328.
 XX PA (GETH) GENENTECH INC.
 XX PI Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 XX PI Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX DR MPI; 2001-381384/40.
 XX DR N-PSDB; AAC85969.
 XX PT Isolated PRO polypeptide useful for treat or diagnose an immune-related
 XX PT disorder e.g. arthritis, asthma, allergy, diabetes or psoriasis -
 XX PS Claim 1; Fig 18; 124pp; English.

XX The sequences given in AAB47291-99 show PRO polypeptides. PRO1081, CC PRO1274 and PRO10272 stimulate the proliferation of T-lymphocytes and CC PRO1599 and PRO1556. PRO4401 and PRO10268 inhibit the proliferation of CC T-lymphocytes. PRO1754 and PRO9912 act to enhance the infiltration of CC mononuclear cells, eosinophils or polymorphonuclear neutrophils (PMN) CC into the tissue of a mammal. The PRO cDNA's and antibodies which CC bind to them, are used to treat an immune-related disorder in a CC mammal. Such disorders include systemic lupus erythematosus, CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a CC sporadic arthropathy, systemic sclerosis, an idiopathic inflammatory CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, CC diabetes mellitus, immune-mediated renal disease, a demyelinating CC disease of the central or peripheral nervous system, idiopathic CC demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic CC inflammatory demyelinating polyneuropathy, a hepatobiliary disease, CC infectious or autoimmune chronic active hepatitis, primary biliary CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's CC disease, an autoimmune or immune-mediated skin disease, a bulous skin CC disease, erythema multiforme, contact dermatitis, psoriasis, an CC allergic disease, asthma, allergic rhinitis, atopic dermatitis, food CC hypersensitivity, urticaria, an immunologic disease of the lung, CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity CC pneumonitis, a transplantation associated disease, graft rejection or CC graft-versus-host disease.

Sequence 177 AA:

Query Match 100.0%; Score 985; DB 22; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.6e-93;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCPSKGDTSSELLRMSTVPVP 60
DB 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCPSKGDTSSELLRMSTVPVP 60
QY 61 PLEPRPNRHPSCRASEDPPLNSRAISPMRYELDRDLNRLPDLVHARCLCPHCYSLOT 120
DB 61 PLEPRPNRHPSCRASEDPPLNSRAISPMRYELDRDLNRLPDLVHARCLCPHCYSLOT 120
QY 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTGKGYCLERRLRVSLACVCPRPVWG 177
DB 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTGKGYCLERRLRVSLACVCPRPVWG 177

RESULT 3
AAB87603
ID AAB87603 standard; Protein: 177 AA.

XX AAB87603;
XX 15-MAY-2001 (first entry)
XX Human PRO10272.
XX Human; PRO protein; mapping.
XX Homo sapiens.
XX MO200116318-A2.
XX 08-MAR-2001.
XX 24-AUG-2000; 2000MO-US23328.
XX 01-SEP-1999; 99MO-US20111.
XX 15-SEP-1999; 99MO-US21090.
XX 07-DEC-1999; 99US-0159495.
XX 09-DEC-1999; 99US-0170262.
XX 11-JAN-2000; 2000US-0175481.
XX 18-FEB-2000; 2000MO-US04341.

PR 18-FEB-2000; 2000MO-US04342.
PR 22-FEB-2000; 2000MO-US04414.
PR 01-MAR-2000; 2000MO-US05601.
PR 03-MAR-2000; 2000US-0187202.
PR 25-APR-2000; 2000US-0199397.
PR 22-MAY-2000; 2000MO-US14042.
PR 05-JUN-2000; 2000US-0209832.
XX (GETH) GENENTECH INC.
XX Eaton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WPL: 2001-183260/18.
DR N-PSDB: AAF92135.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in
PT molecular biology, including use as hybridization probes, and in
PT chromosome and gene mapping.

PS Claim 12; Fig 156; 278bp; English.

XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping.

Sequence 177 AA:

Query Match 100.0%; Score 985; DB 22; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.6e-93;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCPSKGDTSSELLRMSTVPVP 60
DB 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCPSKGDTSSELLRMSTVPVP 60
QY 61 PLEPRPNRHPSCRASEDPPLNSRAISPMRYELDRDLNRLPDLVHARCLCPHCYSLOT 120
DB 61 PLEPRPNRHPSCRASEDPPLNSRAISPMRYELDRDLNRLPDLVHARCLCPHCYSLOT 120
QY 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTGKGYCLERRLRVSLACVCPRPVWG 177
DB 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTGKGYCLERRLRVSLACVCPRPVWG 177

RESULT 4
AAB07598
ID AAB07598 standard; Protein: 161 AA.

XX AAB07598;
XX 07-NOV-2000 (first entry)
XX A human interleukin (IL) 174 polypeptide.
XX Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
XX IL-177; IL-171; cell proliferation; cancer.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..16
FT Modified-site /note- "signal peptide"
FT Modified-site 15..17
FT Modified-site /note- "calcium phosphorylation site"
FT Modified-site 16..18
FT Modified-site /note- "calcium phosphorylation site"
FT Modified-site 12..16

FT Protein /note- "myristoylation site"
 FT 17..161
 FT /note- "mature protein"
 FT 21
 FT Modified-site /note- "phosphorylation site"
 FT 21..24
 FT Modified-site /note- "CAMP protein kinase phosphorylation site"
 FT 23
 FT Modified-site /note- "phosphorylation site"
 FT 41..43
 FT Modified-site /note- "protein kinase C phosphorylation site"
 FT 43
 FT Modified-site /note- "phosphorylation site"
 FT 45..47
 FT Modified-site /note- "calcium phosphorylation site"
 FT 53
 FT Modified-site /note- "phosphorylation site"
 FT 53..56
 FT Modified-site /note- "CAMP protein kinase phosphorylation site"
 FT 56
 FT Modified-site /note- "phosphorylation site"
 FT 95
 FT Modified-site /note- "phosphorylation site"
 FT 95..98
 FT Modified-site /note- "CAMP protein kinase phosphorylation site"
 FT 95..102
 FT Modified-site /note- "tyrosine kinase site"
 FT 98
 FT Modified-site /note- "phosphorylation site"
 FT 104..107
 FT Modified-site /note- "N-glycosylation site"
 FT 115..119
 FT Modified-site /note- "myristoylation site"
 FT 118..122
 FT Modified-site /note- "myristoylation site"
 FT 119..121
 FT Modified-site /note- "protein kinase C phosphorylation site"
 FT 131
 FT Modified-site /note- "phosphorylation site"
 FT /note- "phosphorylation site"
 PN W0200042188-A2.
 XX 20-JUL-2000.
 XX 10-JAN-2000; 2000MO-US00006.
 XX 11-JAN-1999; 99US-0228822.
 XX (SCHE) SCHERING CORP.
 XX Gorman DM, Bazan JF, Kastelein RA;
 XX WPI: 2000-466130/40.
 DR N-PSDB: AAS58986.
 XX
 PT New isolated polynucleotide encoding a mammalian Interleukin-17 like
 XX protein used to identify genes for homologous proteins -
 PS Claim 11; Page 16; 111pp; English.
 XX
 CC The present sequence represents an interleukin-174 (IL-174) polypeptide.
 CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
 CC member of a new group of interleukins, IL-170 polypeptides. The members
 CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
 CC protein can be used to treat abnormal proliferation e.g. cancer
 CC or degenerative conditions. Antibodies can be used in diagnostic
 CC methods to detect over production of IL-170 protein in cells or body
 CC fluids.
 XX
 SQ Sequence 161 AA;
 Query Match 91.2%; Score 898; DB 21; Length 161;
 Best local Similarity 100.0%; Pred. No. 2.1e-84;

Matches	159; Conservative	0; Mismatches	0; Indels
QY 19	QYVAFIANYMGTHHTYSHWSPCCPSKQODTSEELLRMSTVVPLEPARPRHPSCHASE 78		
Db 3	QYVAFIANYMGTHHTYSHWSPCCPSKQODTSEELLRMSTVVPLEPARPRHPSCHASE 62		
QY 79	DGPLNSRAISPMRYELDRDLNRLPOLYHARCICPHCVSLQTSQSHMDPRNSSELLYHNOT 138		
Db 63	DGPLNSRAISPMRYELDRDLNRLPOLYHARCICPHCVSLQTSQSHMDPRNSSELLYHNOT 122		
QY 139	VFYRRPCHEKGTNKGVCLEERLYRVSLACVCPRPVWG 177		
Db 123	VFYRRPCHEKGTNKGVCLEERLYRVSLACVCPRPVWG 161		
RESULT 5			
AAB07692			
ID	AAB07692 standard; Protein; 161 AA.		
XX	AAB07692;		
XX	07-NOV-2000 (first entry)		
DE	A human interleukin-174 polypeptide.		
XX	Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;		
KM	IL-174; IL-176; IL-177; cell proliferation; cancer.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	Peptide		
FT	Location/Qualifiers		
FT	1..16		
FT	/note- "signal peptide"		
FT	15..17		
FT	/note- "calcium phosphorylation site"		
FT	16..18		
FT	/note- "calcium phosphorylation site"		
FT	12..16		
FT	/note- "myristoylation site"		
FT	17..161		
FT	/note- "mature protein"		
FT	21		
FT	/note- "phosphorylation site"		
FT	21..24		
FT	/note- "CAMP protein kinase phosphorylation site"		
FT	23		
FT	/note- "phosphorylation site"		
FT	41..43		
FT	/note- "protein kinase C phosphorylation site"		
FT	43		
FT	/note- "phosphorylation site"		
FT	45..47		
FT	/note- "calcium phosphorylation site"		
FT	53		
FT	/note- "phosphorylation site"		
FT	53..56		
FT	/note- "CAMP protein kinase phosphorylation site"		
FT	56		
FT	/note- "phosphorylation site"		
FT	95		
FT	/note- "phosphorylation site"		
FT	95..98		
FT	/note- "CAMP protein kinase phosphorylation site"		
FT	95..102		
FT	/note- "tyrosine kinase site"		
FT	98		
FT	/note- "phosphorylation site"		
FT	104..107		
FT	/note- "N-glycosylation site"		
FT	115..119		
FT	/note- "myristoylation site"		
FT	118..122		
FT	/note- "myristoylation site"		

```

FT Modified-site 119..121
FT /note="protein kinase C phosphorylation site"
FT Modified-site 131
FT /note="phosphorylation site"
XX MO200042187-A1.
XX 20-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US00005.
XX
XX 11-JAN-1999; 99US-0229402.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Bazan JF, Kastelein RA;
XX
XX WPI; 2000-476060/41.
XX
XX N-PSDB; AAS59158.
XX
XX
XX New DNA sequence encoding a mammalian homolog of CTLA-8, designated
XX Interleukin-171 (IL-171), useful for recombinant production of IL-171
XX physiology or development.
XX
XX Disclosure; Page 19; 11pp; English.
XX
XX
XX The present sequence represents an Interleukin (IL)-174 polypeptide.
XX It is a mammalian homologue of the cytokine designated CTLA-8 (also
XX referred to as IL-17). The specification also describes homologues
XX IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA
XX sequence encoding IL-171 is useful for identifying genes, mRNA and
XX cDNA molecules which code for related or homologous proteins. The
XX IL-171 protein, antibodies against IL-171, and compounds which have
XX binding affinity to IL-171 are useful in treatment of conditions
XX associated with abnormal physiology or development, including abnormal
XX proliferation, e.g., cancerous conditions, or degenerative conditions.
XX The IL-171 protein can be used in kits and assay methods for identifying
XX compounds that selectively bind to IL-171.
XX
XX Sequence 161 AA:
SQ
Query Match 91.2%; Score 898; DB 21; Length 161;
Best Local Similarity 100.0%; Pred. No. 2,1e-84;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPVPLPARPNRHPESCRASE 78
DB 3 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPVPLPARPNRHPESCRASE 62
QY 79 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCICPHCVSLQTSQSHMDPRGNSSELLYHNQT 138
DB 63 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCICPHCVSLQTSQSHMDPRGNSSELLYHNQT 122
QY 139 VFYRPPCHGEKGTTHKGYCLERRLRYVSLACVCPVRRVWG 177
DB 123 VFYRPPCHGEKGTTHKGYCLERRLRYVSLACVCPVRRVWG 161

```

```

KW Infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;
KW cancer.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..16
XX FT /label= Signal_peptide
XX FT Protein 17..161
XX FT /label= Mature_IL-17L_protein
XX
XX WO200208285-A2.
XX
XX 31-JAN-2002.
XX
XX
XX 21-JUN-2001; 2001WO-US19861.
XX
XX PF 22-JUN-2000; 2000US-213125P.
XX PR 02-FEB-2001; 2001US-266159P.
XX PR 16-MAR-2001; 2001US-0810384.
XX
XX (AMGE-) AMGEN INC.
XX
XX Medlock E, Yeh R, Silbiger SM, Elliott GS, Nguyen HQ, Jing S;
XX WPI; 2002-155217/20.
XX N-PSDB; AAD28771.
XX
XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
XX polypeptides useful in the treatment, prevention and diagnosis of
XX diseases e.g. cancer.
XX
XX Claim 13; Fig 1; 242pp; English.
XX
XX The invention relates to nucleic acid molecules encoding Interleukin 17
XX (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
XX of IL-17 protein in an animal. The IL-17 protein is useful for treating
XX preventing or ameliorating a disease, such as immune system dysfunction
XX (rheumatoid arthritis, osteoarthritis, inflammatory joint disease)
XX autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
XX disease, transplant rejection, graft vs. host disease). Infections (HIV,
XX hepatitis, bacterial), weight disorders (obesity, anorexia, cachexia,
XX sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
XX (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
XX (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
XX (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
XX atherosclerosis, heart failure, angiogenesis); tumours; cancers (lymphoma
XX leukaemia); reproductive (infertility, miscarriage, endometriosis), eye
XX blindness, retinal neuropathy) and treatment of diseases involving
XX inflammation. The present sequence is human Interleukin-17 like (IL-17L)
XX protein.
XX
XX Sequence 161 AA:
SQ
Query Match 91.2%; Score 898; DB 23; Length 161;
Best Local Similarity 100.0%; Pred. No. 2,1e-84;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPVPLPARPNRHPESCRASE 78
DB 3 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPVPLPARPNRHPESCRASE 62
QY 79 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCICPHCVSLQTSQSHMDPRGNSSELLYHNQT 138
DB 63 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCICPHCVSLQTSQSHMDPRGNSSELLYHNQT 122
QY 139 VFYRPPCHGEKGTTHKGYCLERRLRYVSLACVCPVRRVWG 177
DB 123 VFYRPPCHGEKGTTHKGYCLERRLRYVSLACVCPVRRVWG 161

```


disorders involving aberrant protein expression or biological activity.

Modified-site	64	/note="cAMP protein kinase phosphorylation site"
---------------	----	--

Modified date	note="
01.04	"CAMP protein kinase phosphorylation sites"

```

/notes="phosphorylation site"

```


IL-17 protein, antibodies against IL-17, and compounds which have binding affinity to IL-17 are useful in treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The IL-17 protein can be used in kits and assay methods for identifying compounds that selectively bind to IL-17.

Sequence 169 AA:

Query Match 70.8%; Score 697; DB 21; Length 169;
Best Local Similarity 76.5%; Pred. No. 1.1e-63;
Matches 127; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

19 QVAFVFLAMVMTHTY-----SHWPCSCPSGQDTSELLRMSTVPPLEPARPNR 70
3 QVAFVFLAMVGTHTVSLRIQEGCSHLPCSCPEQEPPEMLKWSASVSPPEPLSHTH 62
71 PESCRASEDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSGHMDPRGNS 130
63 AESCRASKDGPLNSRAISPMRYELDRDLNRPDLYHARCICPHCVSLQTSGHMDPLGNS 122
131 ELLYHNOVTFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRRVM 176
123 VPLVHNOVTFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRRVM 168

RESULT 12
AAE18121
ID AAE18121 standard; Protein; 169 AA.

AAE18121;

07-MAY-2002 (first entry)

Mouse Interleukin-17 like (IL-17L) protein.

Mouse; Interleukin-17 like; IL-17L; immune system dysfunction; diabetes; cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema; eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis; leukodema; retinal neuropathy; infertility; miscarriage; inflammation; cancer.

Mus musculus.

Key Location/Qualifiers

Peptide 1..18 /label= Signal_peptide

Protein 19..169 /label= Mature_IL_17L_protein

MO200208285-A2.

31-JAN-2002.

21-JUN-2001; 2001WO-US19861.

22-JUN-2000; 2000US-21125P.

02-FEB-2001; 2001US-266159P.

16-MAR-2001; 2001US-0810384.

(AMGE-) AMGEN INC.

Medlock E, Yeh R, Silbiger SM, Elliott GS, Nguyen HQ, Jing S;

WPI; 2002-155217/20.

N-PSDB; AAD28772.

Nucleic acid molecules encoding Interleukin 17 (IL-17) - like

polypeptides useful in the treatment, prevention and diagnosis of diseases e.g. cancer -

Claim 13; Fig 2; 242pp; English.

The invention relates to nucleic acid molecules encoding Interleukin 17 (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels of IL-17 protein in an animal. The IL-17 protein is useful for treating, preventing or ameliorating a disease, such as immune system dysfunction (rheumatoid arthritis, osteoarthritis, inflammatory joint disease), autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, graft vs. host disease), infections (HIV, hepatitis, bacterial), weight disorders (obesity, anorexia, cachexia, sepsis), neuronal dysfunction (Alzheimer's, Parkinson's disease), lung (acute respiratory distress syndrome, cystic fibrosis, emphysema), skin (psoriasis, eczema, wound healing), kidney (glomerulonephritis), bone (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy atherosclerosis, heart failure, angiodysplasia), tumours, cancers (lymphoma leukaemia), reproductive (infertility, miscarriage, endometriosis), eye (blindness, retinal neuropathy) and treatment of diseases involving inflammation. The present sequence is mouse Interleukin-17 like (IL-17L) protein.

Sequence 169 AA:

Query Match 70.8%; Score 697; DB 23; Length 169;
Best Local Similarity 76.5%; Pred. No. 1.1e-63;
Matches 127; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

19 QVAFVFLAMVMTHTY-----SHWPCSCPSGQDTSELLRMSTVPPLEPARPNR 70
3 QVAFVFLAMVGTHTVSLRIQEGCSHLPCSCPEQEPPEMLKWSASVSPPEPLSHTH 62
71 PESCRASEDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSGHMDPRGNS 130
63 AESCRASKDGPLNSRAISPMRYELDRDLNRPDLYHARCICPHCVSLQTSGHMDPLGNS 122
131 ELLYHNOVTFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRRVM 176
123 VPLVHNOVTFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRRVM 168

RESULT 13

AAM52692 standard; Protein; 169 AA.

AAM52692;

26-FEB-2002 (first entry)

Murine Interleukin 174 (IL-174).

Mouse; murine; Interleukin 174; IL-174; cytokine; Th2 response; innate immune response; inflammation; gut cell growth; extramedullary haematopoiesis; antibody response; granuloma formation; autoimmune condition; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; diabetes; psoriasis; infectious agent; inflammatory condition; Crohn's disease; ulcerative colitis; pancreatitis; hepatitis; allergy; Th2-mediated condition; systemic anaphylactic response; skin hypersensitivity response; dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator; antiinflammatory; antiarthritic; antidiabetic; antifungal; dermatological; neuroprotective; antiallergic; agonist; antagonist.

Mus sp.

Key Location/Qualifiers

Peptide 1..16 /label= Signal_peptide

Protein 17..169 /label= Mature_IL-174

MO200179288-A2.

ID AAB07599 standard; Protein: 144 AA.
 XX AAB07599;
 AC
 XX 07-NOV-2000 (first entry)
 DT
 XX A murine Interleukin (IL) 174 polypeptide.
 DE
 XX Interleukin: IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
 KM IL-177; IL-171; cell proliferation; cancer.
 XX
 OS Mus sp.
 XX
 XX WO200042188-A2.
 PN
 XX 20-JUL-2000.
 PD
 XX 10-JAN-2000; 2000WO-US00006.
 PF
 XX 11-JAN-1999; 99US-0228822.
 PR
 XX (SCHE) SCHERING CORP.
 PA
 XX Gorman DM, Bazan JF, Kastelein RA;
 PI
 XX WPI: 2000-466130/40.
 DR
 XX N-PSDB; AAB58987.
 DR
 XX
 PT New isolated polynucleotide encoding a mammalian Interleukin-17 like
 PT protein used to identify genes for homologous proteins -
 XX
 XX Claim 11; Page 17; 111pp; English.
 PS
 XX
 CC The present sequence represents an Interleukin-174 (IL-174) polypeptide.
 CC member of a new group of interleukins, IL-170 related protein. It is a
 CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
 CC protein can be used to treat abnormal proliferation e.g. cancer
 CC or degenerative conditions. Antibodies can be used in diagnostic
 CC methods to detect over production of IL-170 protein in cells or body
 CC fluids.
 CC
 XX
 SQ Sequence 144 AA;
 Query Match 35.7%; Score 351.5; DB 21; Length 144;
 Best Local Similarity 59.8%; Pred. No. 3.1e-28;
 Matches 70; Conservative 6; Mismatches 36; Indels 5; Gaps 2;
 QY 59 VPP--LEPARPNRHPESCRAEDGPLNSRAISPMRYELDRDLNRLPODLYHARCLCPHCY 116
 DB 19 IPRASEPPEPRR---ILQCGQGWPLNSRAISPMRYELDRDLNRLPODLYHARCLCPHCY 75
 QY 117 SLDTGSHMDPRGNSSELYHNQTVFYRRPCHGEKGTGKGYCLERRLYRVSILACVCVRP 173
 DB 76 TLDTGSHMDPLGNVSPLYHNQTVFYRRPCHMARVPIAATAWSAGLPSILGLCVCAAP 132

Search completed: February 26, 2003, 09:31:37
 Job time : 37 secs

Protein 17..161 /note- "myristoylation site"
 Modified-site 21 /note- "mature protein"
 Modified-site 21..24 /note- "phosphorylation site"
 Modified-site 23 /note- "CAMP protein kinase phosphorylation site"
 Modified-site 41..43 /note- "phosphorylation site"
 Modified-site 43 /note- "protein kinase C phosphorylation site"
 Modified-site 45..47 /note- "phosphorylation site"
 Modified-site 53 /note- "calcium phosphorylation site"
 Modified-site 53..56 /note- "phosphorylation site"
 Modified-site 56 /note- "CAMP protein kinase phosphorylation site"
 Modified-site 95 /note- "phosphorylation site"
 Modified-site 95..98 /note- "phosphorylation site"
 Modified-site 95..102 /note- "CAMP protein kinase phosphorylation site"
 Modified-site 98 /note- "tyrosine kinase site"
 Modified-site 104..107 /note- "phosphorylation site"
 Modified-site 115..119 /note- "N-glycosylation site"
 Modified-site 118..122 /note- "myristoylation site"
 Modified-site 119..121 /note- "myristoylation site"
 Modified-site 131 /note- "protein kinase C phosphorylation site"
 Modified-site 131 /note- "phosphorylation site"

2000042188-A2.

20-JUL-2000.

U-JAN-2000; 2000MO-US00006.

AN-1999; 99US-0228822.

() SCHERING CORP.

Man DM, Bazan JF, Kastelein RA;

2000-466130/40.

db; AAS8986.

isolated polynucleotide encoding a mammalian Interleukin-17 like
 used to identify genes for homologous proteins

11; Page 16; 11pp; English.

present sequence represents an interleukin-174 (IL-174) polypeptide.
 peptide is an IL-17-like (CTLA-8 related) protein. It is a
 of a new group of interleukins, IL-170 polypeptides. The members
 IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
 can be used to treat abnormal proliferation e.g. cancer
 inductive conditions. Antibodies can be used in diagnostic
 to detect over production of IL-170 protein in cells or body

161 AA.

91.28; Score 898; DB 21; Length 161;
 100.0%; Pred. No. 2.1e-84;

Matches	159; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
Qy	19 QVAFIAMVMTHTYSHMPSCPSGGDTSEELRSTVPPLEPARNRPESCRAE 78				
Db	3 QVAFIAMVMTHTYSHMPSCPSGGDTSEELRSTVPPLEPARNRPESCRAE 78				
Qy	79 DGPLNSRAISPMRYELDRDLRPLDLYHACLCPCVSLQTSMDPRGSELYHNQT 138				
Db	63 DGPLNSRAISPMRYELDRDLRPLDLYHACLCPCVSLQTSMDPRGSELYHNQT 138				
Qy	139 VFYRPOHGEKGTGKCYCLERRLYRVSILACVAPRYMG 177				
Db	123 VFYRPOHGEKGTGKCYCLERRLYRVSILACVAPRYMG 161				
RESULT 5					
AAB07692					
ID AAB07692 standard; Protein; 161 AA.					
AC					
XX					
DT	07-NOV-2000 (first entry)				
XX					
DE	A human Interleukin-174 polypeptide.				
XX					
KM	Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;				
KW	IL-174; IL-176; IL-177; cell proliferation; cancer.				
OS	Homo sapiens.				
XX					
XX					
Key	Location/Qualifiers				
FT	Peptide				
FT	1..16				
FT	/note- "signal peptide"				
FT	15..17				
FT	/note- "calcium phosphorylation site"				
FT	16..18				
FT	/note- "calcium phosphorylation site"				
FT	12..16				
FT	/note- "myristoylation site"				
FT	17..161				
FT	/note- "mature protein"				
FT	21				
FT	/note- "phosphorylation site"				
FT	21..24				
FT	/note- "CAMP protein kinase phosphorylation site"				
FT	23				
FT	/note- "phosphorylation site"				
FT	41..43				
FT	/note- "protein kinase C phosphorylation site"				
FT	43				
FT	/note- "phosphorylation site"				
FT	45..47				
FT	/note- "calcium phosphorylation site"				
FT	53				
FT	/note- "phosphorylation site"				
FT	53..56				
FT	/note- "CAMP protein kinase phosphorylation site"				
FT	56				
FT	/note- "phosphorylation site"				
FT	95				
FT	/note- "phosphorylation site"				
FT	95..98				
FT	/note- "CAMP protein kinase phosphorylation site"				
FT	95..102				
FT	/note- "tyrosine kinase site"				
FT	98				
FT	/note- "phosphorylation site"				
FT	104..107				
FT	/note- "N-glycosylation site"				
FT	115..119				
FT	/note- "myristoylation site"				
FT	118..122				
FT	/note- "myristoylation site"				

05 FT Modified-site 119..121
 04 FT /note="protein kinase C phosphorylation site"
 03 FT Modified-site 131
 02 FT /note="phosphorylation site"
 01 FT MO200042187-A1.
 00 PD 20-JUL-2000.
 00 PD 10-JAN-2000; 2000WO-US00005.
 00 PD 11-JAN-1999; 990US-0229402.
 00 PD (SCHE) SCHERING CORP.
 00 PD Gorman DM, Bazan JF, Kastelein RA;
 00 PD WPI: 2000-476060/41.
 00 PD N-PSDB; AAA59158.
 00 PD
 00 PD New DNA sequence encoding a mammalian homolog of CTLA-8, designated
 00 PD Interleukin-171 (IL-171), useful for recombinant production of IL-171
 00 PD physiology or development
 00 PD
 00 PD Disclosure: Page 19; 11pp; English.
 00 PD
 00 PD The present sequence represents an interleukin (IL)-174 polypeptide.
 00 PD It is a mammalian homologue of the cytokine designated CTLA-8 (also
 00 PD referred to as IL-17). The specification also describes homologues
 00 PD IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA
 00 PD sequence encoding IL-171 is useful for identifying genes, mRNA and
 00 PD cDNA molecules, which code for related or homologous proteins. The
 00 PD IL-171 protein, antibodies against IL-171, and compounds which have
 00 PD binding affinity to IL-171 are useful in treatment of conditions
 00 PD associated with abnormal physiology or development, including abnormal
 00 PD proliferation, e.g. cancerous conditions, or degenerative conditions.
 00 PD The IL-171 protein can be used in kits and assay methods for identifying
 00 PD compounds that selectively bind to IL-171.
 00 PD
 00 PD Sequence 161 AA;
 00 PD
 00 PD Query Match
 00 PD Best Local Similarity 91.2%; Score 898; DB 21; Length 161;
 00 PD Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 00 PD
 00 PD 19 QVAFLLAMVGTHTYSHMPCSCPKGDTSELLRMSTVPPVPLEPARNHRESCRASE 78
 00 PD 3 QVAFLLAMVGTHTYSHMPCSCPKGDTSELLRMSTVPPVPLEPARNHRESCRASE 62
 00 PD 79 DGPLNSRAISPMRYEELDRDLNRLPQDLVHARCLCPHCVSLQTSQSHMPRGNSSELLYHNOT 138
 00 PD 63 DGPLNSRAISPMRYEELDRDLNRLPQDLVHARCLCPHCVSLQTSQSHMPRGNSSELLYHNOT 122
 00 PD 139 VFYRRPCHGEKGTGKGYCLERRLRYSLACVCPRPVWG 177
 00 PD 123 VFYRRPCHGEKGTGKGYCLERRLRYSLACVCPRPVWG 161
 00 PD
 00 PD RESULT 6
 00 PD ID AAE18120
 00 PD AC AAE18120;
 00 PD
 00 PD 17-MAY-2002 (first entry)
 00 PD
 00 PD Interleukin-17 like (IL-17L) protein.
 00 PD
 00 PD Interleukin-17 like; IL-17L; immune system dysfunction; diabetes;
 00 PD rheumatoid arthritis; therapy; lupus;
 00 PD disease; neuronal dysfunction; transplacental rejection;
 00 PD eye; skin; kidney; bone; eye; vascular system;

KW Infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
 KW epilepsy; atherosclerosis; heart failure; angiodysplasia; Paget's disease;
 KW leukemia; retinal neuropathy; infertility; miscarriage; inflammation;
 KW cancer.
 OS Homo sapiens.
 FH Key
 FT Peptide 1..16
 FT /label= signal_peptide
 FT Protein 17..161
 FT /label= Mature_IL-17L_protein
 PN WO200208285-A2.
 PD 31-JAN-2002.
 PD 21-JUN-2001; 2001WO-US19861.
 PD 22-JUN-2000; 2000US-213125P.
 PD 02-FEB-2001; 2001US-266159P.
 PD 16-MAR-2001; 2001US-0810384.
 PD (AMGE-) AMGEN INC.
 PD Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;
 PD WPI: 2002-155217/20.
 PD N-PSDB; AAD28771.
 PD
 PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
 PT polypeptides useful in the treatment, prevention and diagnosis of
 PT diseases e.g. cancer
 PS Claim 13; Fig 1; 242pp; English.
 CC
 CC The invention relates to nucleic acid molecules encoding Interleukin 17
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,
 CC preventing or ameliorating a disease, such as immune system dysfunction
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease),
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
 CC atherosclerosis, heart failure, angiodysplasia); tumors, cancers (lymphoma
 CC leukemia); reproductive (infertility, miscarriage, endometriosis); eye
 CC inflammation. The present sequence is human Interleukin-17 like (IL-17L)
 CC protein.
 CC
 CC Sequence 161 AA;
 CC
 CC Query Match
 CC Best Local Similarity 91.2%; Score 898; DB 23; Length 161;
 CC Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 19 QVAFLLAMVGTHTYSHMPCSCPKGDTSELLRMSTVPPVPLEPARNHRESCRASE 78
 CC 3 QVAFLLAMVGTHTYSHMPCSCPKGDTSELLRMSTVPPVPLEPARNHRESCRASE 62
 CC 79 DGPLNSRAISPMRYEELDRDLNRLPQDLVHARCLCPHCVSLQTSQSHMPRGNSSELLYHNOT 138
 CC 63 DGPLNSRAISPMRYEELDRDLNRLPQDLVHARCLCPHCVSLQTSQSHMPRGNSSELLYHNOT 122
 CC 139 VFYRRPCHGEKGTGKGYCLERRLRYSLACVCPRPVWG 177
 CC 123 VFYRRPCHGEKGTGKGYCLERRLRYSLACVCPRPVWG 161
 CC

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:31:41 ; Search time 14 Seconds
(without alignments)
371.990 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985
Sequence: 1 MRERRRGEDESSLSLFLQV.....ERRLYRSLACVCPRYWG 177

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/PCBUS.COMB.pep:*
7: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	12.4	153	1	US-08-514-014-12 Sequence 12, Appl
2	122	12.4	153	2	US-08-833-823-12 Sequence 12, Appl
3	122	12.4	163	3	US-09-034-810-2 Sequence 2, Appl
4	122	12.4	163	3	US-08-685-239-2 Sequence 2, Appl
5	121	12.3	205	4	US-09-724-864-37 Sequence 37, Appl
6	105.5	10.7	155	4	US-08-432-994A-8 Sequence 8, Appl
7	93.5	9.5	151	2	US-08-620-694A-8 Sequence 8, Appl
8	93.5	9.5	151	3	US-09-034-810-6 Sequence 8, Appl
9	93.5	9.5	151	3	US-09-022-255-8 Sequence 8, Appl
10	93.5	9.5	151	3	US-09-022-255-8 Sequence 8, Appl
11	93.5	9.5	151	3	US-08-685-239-6 Sequence 8, Appl
12	93.5	9.5	151	3	US-09-022-253-8 Sequence 8, Appl
13	93.5	9.5	151	3	US-09-022-253-8 Sequence 8, Appl
14	93.5	9.5	151	3	US-09-022-253-8 Sequence 8, Appl
15	93.5	9.5	151	4	US-09-022-257-8 Sequence 8, Appl
16	93.5	9.5	151	4	US-08-432-994A-4 Sequence 4, Appl
17	91	9.2	150	3	US-09-034-810-4 Sequence 4, Appl
18	91	9.2	150	3	US-08-685-239-4 Sequence 4, Appl
19	91	9.2	150	4	US-08-432-994A-2 Sequence 4, Appl
20	91	9.2	150	4	US-08-432-994A-10 Sequence 10, Appl
21	86	8.7	158	2	US-08-620-694A-7 Sequence 7, Appl
22	86	8.7	158	2	US-09-022-255-7 Sequence 7, Appl
23	86	8.7	158	3	US-09-022-255-7 Sequence 7, Appl
24	86	8.7	158	3	US-09-022-255-7 Sequence 7, Appl
25	86	8.7	158	3	US-09-022-255-7 Sequence 7, Appl
26	86	8.7	158	3	US-09-022-255-7 Sequence 7, Appl
27	86	8.7	158	4	US-09-022-257-7 Sequence 7, Appl

28	77.5	7.9	961	5	PCR-US93-11225-4	Sequence 4, Appl
29	76.5	7.8	1323	1	US-08-026-138E-4	Sequence 4, Appl
30	75.5	7.7	1185	4	US-08-664-962B-2	Sequence 2, Appl
31	75.5	7.7	1185	4	US-09-311-743-2	Sequence 2, Appl
32	75	7.6	514	4	US-08-974-549A-605	Sequence 605, App
33	74.5	7.6	807	4	US-08-974-549A-5	Sequence 5, App
34	74.5	7.6	1132	3	US-08-851-843A-225	Sequence 225, App
35	74.5	7.6	1132	4	US-08-974-549A-2	Sequence 225, App
36	74.5	7.6	1132	4	US-08-974-549A-344	Sequence 344, App
37	74.5	7.6	1132	4	US-08-854-050-225	Sequence 225, App
38	74.5	7.6	1132	4	US-09-430-323-225	Sequence 225, App
39	74.5	7.6	1132	4	US-09-128-354-2	Sequence 225, App
40	74.5	7.6	1132	4	US-09-675-321-2	Sequence 2, Appl
41	74.5	7.6	1132	4	US-08-052-919-2	Sequence 2, Appl
42	74.5	7.6	1132	4	US-08-974-549A-611	Sequence 611, App
43	74.5	7.6	1189	4	US-08-974-549A-613	Sequence 613, App
44	74.5	7.6	1200	4	US-08-974-549A-612	Sequence 612, App
45	74.5	7.6	1285	4	US-08-974-549A-600	Sequence 600, App

ALIGNMENTS

RESULT 1
US-08-514-014-12

Sequence 12, Application US/08514014
Patent No. 5707829

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/514,014

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G16000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 153 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-514-014-12

Query Match 12.4%, Score 122; DB 1; Length 153;

Best Local Similarity 26.2%, Pred. No. 6.6e-06;

Matches 45; Conservative 25; Mismatches 60; Indels 42; Gaps 8;

12 SLISLFLQVVAFLAMVGTHTSYWPCSCGKODTSELLRWSTVVP-----PLEPAR 66

8 SILGLAFLEAFAARKIRPVGHFTFOKPSPC-----PVPGSGMKLDIGI 51

APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, Mckeough
APPLICANT: Goldman, Samuel
APPLICANT: Pltman, Debra
APPLICANT: Mi, Sha
APPLICANT: Neben, Steven
APPLICANT: Giannotti, Joann
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,239
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-239-2

Query Match
Best Local Similarity 26.4%; Score 122; DB 3; Length 163;
Matches 45; Conservative 25; Mismatches 60; Indels 42; Gaps 8;

QY 12 SLISL-FLQVAVFLAMVGTHTSHMPSGQDTSSELLRMSTVVP-PLFEPAR 66
18 SLIGLAFLEAARKIKVGHTEFOKPESCP-----PVPGSMKLDIGI 61
QY 67 PRRHPSCRASEDGPLNRAISPMRYELDRNLRLPDOLYHARCPCPVSLQTSMDP 126
62 IN---ENQVSMRNEISTSPMNTVTMDPRRYSEVVOQCRNIGCINAO----- 111
QY 127 RGNSELLYN-----QTVFRRPCHEGKTHKGYCLERRLYRLACVCP 173
112 -GKEDISNVSPIQOETLVVRRK---HGGGSVGFQLEKVL-VTVGCTCTP 157
DB

RESULT 5
US-09-724-864-37
Sequence 37, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Murlison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
FILE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 205
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-37

Query Match
Best Local Similarity 27.1%; Score 121; DB 4; Length 205;
Matches 42; Conservative 19; Mismatches 58; Indels 36; Gaps 7;

QY 41 PSKQDTSSELLR-----WSTVPPELEPARPRHPSCRASE---DGPLN 83
35 PROCADREELLEDQYGLAGVLSAFHHTLQIGREQARNASCAGGAADRRPRPTN 94
QY 84 SRAISPMRYELDRNLRLPDOLYHARCPCPVSLQTSMDPNSSELLYNQVVF--- 140
95 LRSVPMAYRSTYPPARPRYLPEAYCLCRCL---TGLY-----GEEDFRSTVFSPA 147
QY 141 -YRR--PCHGKTHKGYCLERRLYRLACVCP 171
148 VVLRRTAACAGGSGVVAEHT-----TIPVCTCTV 177
DB

RESULT 6
US-08-432-994A-8
Sequence 8, Application US/08432994A
Patent No. 6274711
GENERAL INFORMATION:
APPLICANT: Goistein, Pierre
APPLICANT: Rouvier, Eric
APPLICANT: Fossiez, Francois
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Djossou, Odile
APPLICANT: Banchereau, Jacques
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND
RELATED REAGENTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,994A
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/250,846
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,747
FILING DATE: 05-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,203
FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX038K3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids

Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

QY 11 SLSISFLQVAFLLAMVMTHTYSHMPSCCPSKQDTSSEIL-----RMSIVPVPLEPA 65
Db 6 TSLVLLLL--LSIDIVKSEITSACQPPCLANNSPFRSVMYTLSTRNMT-----54
QY 66 RNRHRESCRASDGLPLNSRAISPMRYELDRDLRLPDOLYHARCICPHCVSLQTSQSHMD 125
Db 55 -----SSKRASD---YNNRSTSPWTLHRNEDODRYPYIWEAKCRYLGCYNAD-----99
QY 126 PRGNSELLYHNOTVFRRCPC---HGEKGT HKGYCLERLYRSLACVCVPRPV 175
Db 100 --GNVD--YHMSVPIQGEILVVRKHGQPCPNSFLEKML--VTVGCTVTPIV 147

RESULT 9

US-09-022-255-8
Sequence 8, Application US/09022255
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620.694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538.765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410.535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-09-022-255-8

Query Match 9.5%; Score 93.5; DB 3; Length 151;
Best Local Similarity 23.0%; Pred. No. 0.009;
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

QY 11 SLSISFLQVAFLLAMVMTHTYSHMPSCCPSKQDTSSEIL-----RMSIVPVPLEPA 65
Db 6 TSLVLLLL--LSIDIVKSEITSACQPPCLANNSPFRSVMYTLSTRNMT-----54
QY 66 RNRHRESCRASDGLPLNSRAISPMRYELDRDLRLPDOLYHARCICPHCVSLQTSQSHMD 125
Db 55 -----SSKRASD---YNNRSTSPWTLHRNEDODRYPYIWEAKCRYLGCYNAD-----99
QY 126 PRGNSELLYHNOTVFRRCPC---HGEKGT HKGYCLERLYRSLACVCVPRPV 175
Db 100 --GNVD--YHMSVPIQGEILVVRKHGQPCPNSFLEKML--VTVGCTVTPIV 147

RESULT 10

US-09-022-696-8
Sequence 8, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410.535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-09-022-696-8

Query Match 9.5%; Score 93.5; DB 3; Length 151;
Best Local Similarity 23.0%; Pred. No. 0.009;
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

OY 11 SSLISLFLQVAVFLAMVGHHTYSHMPCSCPSKGDTSSELL-----RMSVVPVPLEPA 65
Best Local Similarity 23.0%; Pred. No. 0.009; DB 3; Length 151;
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;
DB 6 TSLVLL--LSDICVYKSEITSAQTPRCLAANSPFRSVAVTSLIRNMT-----54
OY 66 RPNRHPSCRASBDGPLNSRAISPWRVELDRDLRPLDOLYHARCICPHCVSLQTSQSHMD 125
DB 55 -----SSKRASD---YNNRSTSPWTLHRNEDQDRYPSVWEAKCRYLGCYNAD-----99
OY 126 PRGNSELYHNQVYFRRPC-----HGEKGTHKGYCLERRLYVSLACVCPVPRV 175
DB 100 --GNVD--YHMSVPIQOELVVRKGHPCPNPFRLKML--VTVCCTCVPPIV 147

RESULT 11
US-08-685-239-6
Sequence 6, Application US/08685239
Patent No. 6074849
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Kelleher, Kerry
APPLICANT: Carlio, McKeough
APPLICANT: Goldman, Samuel
APPLICANT: Piltman, Debra
APPLICANT: Mi, Sha
APPLICANT: Neben, Steven
APPLICANT: Giannotti, Joan
APPLICANT: Golden/Fleet, Margaret
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,239
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION/DOCKET NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-239-6

Query Match 9.5%; Score 93.5; DB 3; Length 151;
Best Local Similarity 23.0%; Pred. No. 0.009;
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;
DB 11 SSLISLFLQVAVFLAMVGHHTYSHMPCSCPSKGDTSSELL-----RMSVVPVPLEPA 65
DB 6 TSLVLL--LSDICVYKSEITSAQTPRCLAANSPFRSVAVTSLIRNMT-----54
OY 66 RPNRHPSCRASBDGPLNSRAISPWRVELDRDLRPLDOLYHARCICPHCVSLQTSQSHMD 125
DB 55 -----SSKRASD---YNNRSTSPWTLHRNEDQDRYPSVWEAKCRYLGCYNAD-----99
OY 126 PRGNSELYHNQVYFRRPC-----HGEKGTHKGYCLERRLYVSLACVCPVPRV 175

DB 100 --GNVD--YHMSVPIQOELVVRKGHPCPNPFRLKML--VTVCCTCVPPIV 147

RESULT 12
US-09-022-253-8
Sequence 8, Application US/09022253
Patent No. 6096305
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Sp199s, William
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,253
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694
FILING DATE: 21-MARCH-1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION/DOCKET NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: NO, 6096305 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-09-022-253-8

Query Match 9.5%; Score 93.5; DB 3; Length 151;
Best Local Similarity 23.0%; Pred. No. 0.009;
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;
DB 11 SSLISLFLQVAVFLAMVGHHTYSHMPCSCPSKGDTSSELL-----RMSVVPVPLEPA 65
DB 6 TSLVLL--LSDICVYKSEITSAQTPRCLAANSPFRSVAVTSLIRNMT-----54
OY 66 RPNRHPSCRASBDGPLNSRAISPWRVELDRDLRPLDOLYHARCICPHCVSLQTSQSHMD 125
DB 55 -----SSKRASD---YNNRSTSPWTLHRNEDQDRYPSVWEAKCRYLGCYNAD-----99

OY 126 PRGNSELYHNOVFYRRPC---HGEKTHKGYCLERLYRVS LACVCVPRV 175
DB 100 --GNVD--YHNSVPIQOEILVVRKGHOPCPNSFRLEKML--VTVGCTCVTPIV 147

RESULT 13

US-09-022-260-8
Sequence 8, Application US/09022260
Patent No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
SPRAIN: ORF13
US-09-022-260-8

Query Match 9.5%; Score 93.5; DB 3; Length 151;
Best Local Similarity 23.0%; Pred. No. 0.009;
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

OY 11 SLSISFLQVAFIAMVMTHTYSHWPCPSKGGDTSEEL-----RWSTVPVPLEPA 65
DB 6 TSLVILL--LSIDICIVKSEITSAQTPCLANNSPRSVMTLSIRNMNT----- 54
OY 66 RPNRHPESCRASEDGPLNSAISPMRYELDRDLRPLQDLYHARCCLPHCVSLQTSQSHMD 125
DB 55 -----SSKRAD--YNNRSTSPWTLHRNEDODRPPSVIWEAKCRYLQGVND----- 99
OY 126 PRGNSELYHNOVFYRRPC---HGEKTHKGYCLERLYRVS LACVCVPRV 175

DB 100 --GNVD--YHNSVPIQOEILVVRKGHOPCPNSFRLEKML--VTVGCTCVTPIV 147

RESULT 14

US-09-022-259-8
Sequence 8, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
SPRAIN: ORF13
US-09-022-259-8

Query Match 9.5%; Score 93.5; DB 4; Length 151;
Best Local Similarity 23.0%; Pred. No. 0.009;
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

OY 11 SLSISFLQVAFIAMVMTHTYSHWPCPSKGGDTSEEL-----RWSTVPVPLEPA 65
DB 6 TSLVILL--LSIDICIVKSEITSAQTPCLANNSPRSVMTLSIRNMNT----- 54
OY 66 RPNRHPESCRASEDGPLNSAISPMRYELDRDLRPLQDLYHARCCLPHCVSLQTSQSHMD 125
DB 55 -----SSKRAD--YNNRSTSPWTLHRNEDODRPPSVIWEAKCRYLQGVND----- 99
OY 126 PRGNSELYHNOVFYRRPC---HGEKTHKGYCLERLYRVS LACVCVPRV 175

Db 100 --GNVD--YHMNSVPIQOEILVVRKHQPCPNFLEKML--VTVGCTCTPTIV 147

RESULT 15

US-09-022-257-8

; Sequence 8, Application US/09022257
; Patent No. 6197525

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

TITLE OF INVENTION: No. 6197525el Receptor that binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,257

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 151 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Herpesvirus Saimiri

STRAIN: ORF13

US-09-022-257-8

Query Match

Best Local Similarity 9.5%; Score 93.5; DB 4; Length 151;

Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

QY 11 SLSISLFQVAVFLAMVGTHTYSHMPSCCPSKQDGTSEELL-----RMSTVPVPPLEPA 65

Db 6 TSLVLLLL--LSIDCIYKSETSAQTPECLANNSPFRSVMTLSIRMMNT-----54

QY 66 RPNHRPESCRASEDGLPNSRAISPMRELDRLNRLPDGLYHARCLCPHCVSLQTSQSHMD 125

Db 55 -----SKRRSD--YYNRSTSPMTLHRNEDQDRYPSVIMEAKCRYLGCVANAD-----99

QY 126 PRGNSELLYHQTQVYRPPC---HGEKTHKGYCLERRLYRVSLACVCPVRPV 175

Db 100 --GNVD--YHMNSVPIQOEILVVRKHQPCPNFLEKML--VTVGCTCTPTIV 147

Search completed: February 26, 2003, 09:33:48
Job time: 15 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:31:56 (Search time 14 Seconds
(Without alignments)
476.912 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985
Sequence: 1 MRRPRRLGDSLSLIFLQV.....ERRLYRVSLACVAPRYWG 177

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 174566 seqs, 37721826 residues

Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	985	100.0	177	9	US-09-874-503-6
2	985	100.0	177	9	US-10-000-157-6
3	985	100.0	177	9	US-10-063-547-156
4	985	100.0	177	9	US-09-816-744-6
5	985	100.0	177	9	US-09-747-259-6
6	985	100.0	177	9	US-10-063-616-156
7	985	100.0	177	9	US-10-063-502-156
8	985	100.0	177	12	US-10-006-867-156
9	898	91.2	161	10	US-09-886-404-2
10	697	70.8	169	10	US-09-886-404-4
11	670	68.0	159	10	US-09-886-404-10
12	170.5	17.3	206	10	US-09-854-280-24
13	170.5	17.3	206	10	US-09-854-208-24
14	165.5	16.8	197	9	US-09-874-503-4
15	165.5	16.8	197	9	US-10-000-157-4
16	165.5	16.8	197	9	US-10-036-041-11
17	165.5	16.8	197	9	US-09-320-713-29
18	165.5	16.8	197	9	US-09-816-744-4
19	165.5	16.8	197	9	US-09-747-259-4

ALIGNMENTS

RESULT 1
US-09-874-503-6
Sequence 6, Application US/09874503
Patent No. US20020177188A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hymowitz, Sarah G.
APPLICANT: Tumas, Daniel
APPLICANT: Starovashnik, Melissa A.
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P3(US)
CURRENT APPLICATION NUMBER: US/09/874,503
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/244,072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/213,807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/138,387

20	165.5	16.8	197	9	US-10-035-855-11	Sequence 11, Appl
21	165.5	16.8	197	9	US-10-174-580-448	Sequence 448, App
22	165.5	16.8	197	9	US-10-176-758-448	Sequence 448, App
23	165.5	16.8	197	9	US-10-175-737-448	Sequence 448, App
24	165.5	16.8	197	9	US-10-173-706-448	Sequence 448, App
25	165.5	16.8	197	9	US-10-175-738-448	Sequence 448, App
26	165.5	16.8	197	9	US-10-175-732-448	Sequence 448, App
27	165.5	16.8	197	9	US-10-176-482-448	Sequence 448, App
28	165.5	16.8	197	9	US-10-176-757-448	Sequence 448, App
29	165.5	16.8	197	9	US-10-176-913-448	Sequence 448, App
30	165.5	16.8	197	9	US-10-180-552-448	Sequence 448, App
31	165.5	16.8	197	9	US-10-180-557-448	Sequence 448, App
32	165.5	16.8	197	9	US-09-931-836-111	Sequence 11, Appl
33	165.5	16.8	197	9	US-10-173-700-448	Sequence 448, App
34	165.5	16.8	197	9	US-10-174-572-448	Sequence 448, App
35	165.5	16.8	197	9	US-10-174-579-448	Sequence 448, App
36	165.5	16.8	197	9	US-10-174-582-448	Sequence 448, App
37	165.5	16.8	197	9	US-10-175-739-448	Sequence 448, App
38	165.5	16.8	197	9	US-10-175-740-448	Sequence 448, App
39	165.5	16.8	197	9	US-10-175-743-448	Sequence 448, App
40	165.5	16.8	197	9	US-10-175-748-448	Sequence 448, App
41	165.5	16.8	197	9	US-10-176-488-448	Sequence 448, App
42	165.5	16.8	197	9	US-10-176-492-448	Sequence 448, App
43	165.5	16.8	197	9	US-10-176-747-448	Sequence 448, App
44	165.5	16.8	197	9	US-10-176-750-448	Sequence 448, App
45	165.5	16.8	197	9	US-10-176-985-448	Sequence 448, App

PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: US 60/134,287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/131,022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: US 60/130,232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/113,621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/644,848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/380,142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/380,138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US99/05028
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 6
LENGTH: 177
TYPE: PRT
ORGANISM: Homo Sapien
US-09-874-503-6

Query Match 100.0%; Score 985; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 4,1e-85;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MREPRLEGDSSILSLFLQVAVFLAMVWGHTYSHMPSCCPSRGODTSEELLRKSTVPVP 60
DB 1 MREPRLEGDSSILSLFLQVAVFLAMVWGHTYSHMPSCCPSRGODTSEELLRKSTVPVP 60
QY 61 PLEPARPNHPSRCASSEGPLNSRAISPMRYELDRDLNLPDDLHARCLCPHCVSLQT 120
DB 61 PLEPARPNHPSRCASSEGPLNSRAISPMRYELDRDLNLPDDLHARCLCPHCVSLQT 120
QY 121 GSHMDPRGNSSELLYHNGTYFYRRPCHGEKGTGKGYCLERLRYSLACVCVRPVMG 177

DB 121 GSHMDPRGNSSELLYHNGTYFYRRPCHGEKGTGKGYCLERLRYSLACVCVRPVMG 177

RESULT 2
US-10-000-157-6
Sequence 6, Application US/10000157
Publication No. US20020182673A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hymowitz, Sarah
APPLICANT: Tumas, Daniel
APPLICANT: Starovastnik, Melissa.
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Matanabe, Collin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OR INVENTION: IT-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381AC1P4(US)
CURRENT APPLICATION NUMBER: US/10/000,157
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/172096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/213807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/242837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/244072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/253646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/908827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 6
LENGTH: 177
TYPE: PRT
ORGANISM: Homo Sapien
US-10-000-157-6

Query Match 100.0%; Score 985; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 4, 1e-85;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRERPRGDESSLSIFLQVAVFLAMVGTHTYSHWSPCCPSKQDTSSEILLRMSVYPV 60
DB 1 MRERPRGDESSLSIFLQVAVFLAMVGTHTYSHWSPCCPSKQDTSSEILLRMSVYPV 60
QY 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSIQT 120
DB 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSIQT 120
QY 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGEGKTHKGYCLERRLRYVSLACVCPRVPMG 177
DB 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGEGKTHKGYCLERRLRYVSLACVCPRVPMG 177

RESULT 3
US-10-063-547-156
Sequence 156, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 156
LENGTH: 177
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-547-156

Query Match 100.0%; Score 985; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 4, 1e-85;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRERPRGDESSLSIFLQVAVFLAMVGTHTYSHWSPCCPSKQDTSSEILLRMSVYPV 60
DB 1 MRERPRGDESSLSIFLQVAVFLAMVGTHTYSHWSPCCPSKQDTSSEILLRMSVYPV 60
QY 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSIQT 120
DB 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSIQT 120
QY 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGEGKTHKGYCLERRLRYVSLACVCPRVPMG 177
DB 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGEGKTHKGYCLERRLRYVSLACVCPRVPMG 177

RESULT 4
US-09-816-744-6
Sequence 6, Application US/09816744
Publication No. US20030003546A1
GENERAL INFORMATION:

APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tamas, Daniel
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Matanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P2(US)
CURRENT APPLICATION NUMBER: US/09/816,744
CURRENT FILING DATE: 2001-03-22
Prior Application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 6
LENGTH: 177
TYPE: PRT
ORGANISM: Homo Sapien
US-09-816-744-6

Query Match 100.0%; Score 985; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 4,1e-85;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRPRLGDSLSLFLQVAFVFLAMVGMCTHTYSHMSPCCPSKODTSEELRMSTVPVP 60
1 MRRPRLGDSLSLFLQVAFVFLAMVGMCTHTYSHMSPCCPSKODTSEELRMSTVPVP 60
Db 61 PLEPARPNRHPESCRASEDGPNLSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQT 120
61 PLEPARPNRHPESCRASEDGPNLSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQT 120
Db 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177
121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177
Db 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177

RESULT 5
US-09-747-259-6
Sequence 6, Application US/09747259
Publication No. US20030008615A1

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Tumas, Daniel
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandeker, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P1(US)
CURRENT APPLICATION NUMBER: US/09/747,259
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 09/644,848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 39

SEQ ID NO 6
LENGTH: 177
TYPE: PRT
ORGANISM: Homo Sapien
US-09-747-259-6

Query Match 100.0%; Score 985; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 4,1e-85;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRPRLGDSLSLFLQVAFVFLAMVGMCTHTYSHMSPCCPSKODTSEELRMSTVPVP 60
1 MRRPRLGDSLSLFLQVAFVFLAMVGMCTHTYSHMSPCCPSKODTSEELRMSTVPVP 60
Db 61 PLEPARPNRHPESCRASEDGPNLSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQT 120
61 PLEPARPNRHPESCRASEDGPNLSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQT 120
Db 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177
121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177
Db 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177

RESULT 6
US-10-063-616-156
Sequence 156, Application US/10063616
Publication No. US20030013855A1

GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1320R1C1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 156
LENGTH: 177
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-616-156

Query Match 100.0%; Score 985; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 4,1e-85;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRPRLGDSLSLFLQVAFVFLAMVGMCTHTYSHMSPCCPSKODTSEELRMSTVPVP 60
1 MRRPRLGDSLSLFLQVAFVFLAMVGMCTHTYSHMSPCCPSKODTSEELRMSTVPVP 60
Db 61 PLEPARPNRHPESCRASEDGPNLSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQT 120
61 PLEPARPNRHPESCRASEDGPNLSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQT 120
Db 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177
121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177
Db 121 GSHMDPRGNSSELYHNQTVFYRRPCHGEKGTHTKGYCLERRLRYVSLACVCPRPVWG 177

RESULT 7
US-10-063-502-156
Sequence 156, Application US/10063502
Publication No. US20030023042A1

GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 156
LENGTH: 177
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-502-156

Query Match 100.0%; Score 985; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.1e-85; Indels 0; Gaps 0;
Matches 177; Conservative 0; Mismatches 0

QY 1 MRERPRLEDESSLSLFLQVAVAFAMVWGTHTYSHWSPSCSPSKGQDTSEELLRMSTVVP 60
1 MRERPRLEDESSLSLFLQVAVAFAMVWGTHTYSHWSPSCSPSKGQDTSEELLRMSTVVP 60
DB 1 PLEPRAPRHPESCRASEDGPLNSRAISPMRYELDRDINRLPQDLYHARCLOPHCVSLQ 120
61 PLEPRAPRHPESCRASEDGPLNSRAISPMRYELDRDINRLPQDLYHARCLOPHCVSLQ 120
QY 121 GSHMDPRGNSSELYNQVTFYRPHGEGKTHKGYCLERLYRVSILACYVPRVWG 177
121 GSHMDPRGNSSELYNQVTFYRPHGEGKTHKGYCLERLYRVSILACYVPRVWG 177
DB 121 GSHMDPRGNSSELYNQVTFYRPHGEGKTHKGYCLERLYRVSILACYVPRVWG 177

RESULT 8
US-10-006-867-156
Sequence 156, Application US/10006867
Patent No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT FILING DATE: US/10/006, 867
CURRENT APPLICATION NUMBER: 2001-12-06
PRIOR APPLICATION NUMBER: 60/064215
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088746
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088825
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089553
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090688
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091628
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/096012
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096757
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/096949
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/096959
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/097954
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/097971
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/097979
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101279

PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105881
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/106030
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106856
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108807
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/112419
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112853
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113011
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/112854
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113408
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114223
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/115614
PRIOR FILING DATE: 1999-01-17
PRIOR APPLICATION NUMBER: 60/115527
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/119285
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119287
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/119525
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/120014
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/129122
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/129674
PRIOR FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/199397
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 985; DB 12; Length 177;
Best Local Similarity 100.0%; Pred. No. 4, 1e-85;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRRPRLGDSLSISLFLQVNAFLAMWGTHTYSHMPCSCPGSDTSELLRMSTVPVP 60
DB 1 MRRPRLGDSLSISLFLQVNAFLAMWGTHTYSHMPCSCPGSDTSELLRMSTVPVP 60
OY 61 PLEPARPNRHPSCRSSECGPLNSRAISPMRYELDRDLRLPDLTHARCLPCHVSIOT 120
DB 61 PLEPARPNRHPSCRSSECGPLNSRAISPMRYELDRDLRLPDLTHARCLPCHVSIOT 120
OY 121 GSHMDRGNSLLYHNGTVFYRRPCHGCKTHGKCYCLERLYVSLACVRRPVNG 177
DB 121 GSHMDRGNSLLYHNGTVFYRRPCHGCKTHGKCYCLERLYVSLACVRRPVNG 177

RESULT 9

US-09-886-404-2

Sequence 2, Application US/09886404

Patent No. US20020037524A1

GENERAL INFORMATION: Eugene

APPLICANT: Medlock, Eugene

APPLICANT: Yeh, Richard

APPLICANT: Silbiger, Scott M.

APPLICANT: Elliott, Gary S.

APPLICANT: Nguyen, Hung Q.

APPLICANT: Jing, Shuguan

TITLE OF INVENTION: IL-17 Like Molecules and Uses thereof

FILE REFERENCE: 01017/37128B

CURRENT FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: 09/810,384

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/266,159

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/213,125

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 161

TYPE: PRT

ORGANISM: Homo sapiens

US-09-886-404-2

Query Match

Best Local Similarity 100.0%;

Matches 159; Conservative 0; Mismatches 0;

Score 898; DB 10; Length 161;

Pred. No. 5e-77; 0; Indels 0; Gaps 0;

QY 19 QVAFLLAMVGTHTYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 78
 DB 3 QVAFLLAMVGTHTYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 62
 QY 79 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDRGNSELLYHNO 138
 DB 63 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDRGNSELLYHNO 122
 QY 139 VFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRPVNG 177
 DB 123 VFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRPVNG 161

RESULT 10
 US-09-886-404-4
 ; Sequence 4, Application US/09886404
 ; Patent No. US20020037524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Medlock, Eugene
 ; APPLICANT: Yeh, Richard
 ; APPLICANT: Silbiger, Scott M.
 ; APPLICANT: Elliott, Gary S.
 ; APPLICANT: Nguyen, Hung Q.
 ; APPLICANT: Jiny, Shuguan
 ; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/37128B
 ; CURRENT APPLICATION NUMBER: US/09/886,404
 ; PRIOR FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: 60/810,384
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/266,159
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/213,125
 ; PRIOR FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 169
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-886-404-4

Query Match 70.8%; Score 697; DB 10; Length 169;
 Best Local Similarity 76.5%; Pred. No. 3.4e-58;
 Matches 127; Conservative 9; Mismatches 22; Indels 8; Gaps 1;
 QY 19 QVAFLLAMVGTHTYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 78
 DB 3 QVAFLLAMVGTHTYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 62
 QY 71 PESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDRGN 130
 DB 63 AESCRASKDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDRGN 122
 QY 131 ELLYHNOVFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRPVNG 176
 DB 123 VPLYHNOVFYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRPVNG 168

RESULT 11
 US-09-886-404-10
 ; Sequence 10, Application US/09886404
 ; Patent No. US20020037524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Medlock, Eugene
 ; APPLICANT: Yeh, Richard
 ; APPLICANT: Silbiger, Scott M.
 ; APPLICANT: Elliott, Gary S.
 ; APPLICANT: Nguyen, Hung Q.
 ; APPLICANT: Jiny, Shuguan
 ; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/37128B

CURRENT APPLICATION NUMBER: US/09/886,404
 ; CURRENT FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: 60/810,384
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/266,159
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/213,125
 ; PRIOR FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 159
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-886-404-10

Query Match 68.0%; Score 670; DB 10; Length 159;
 Best Local Similarity 76.1%; Pred. No. 1.1e-55;
 Matches 121; Conservative 9; Mismatches 21; Indels 8; Gaps 1;
 QY 26 NVMGTHTYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 77
 DB 1 NVMGTHTYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 60
 QY 78 EDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDRGNSELLYHNO 137
 DB 61 KDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDRGNSELLYHNO 120
 QY 138 TVYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRPVNG 176
 DB 121 TVYRRPCHGEKGTHTKGYCLERLYRVSLACVCPRPVNG 159

RESULT 12
 US-09-854-280-24
 ; Sequence 24, Application US/09854280
 ; Patent No. US20020052027A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C2
 ; CURRENT APPLICATION NUMBER: US/09/854,280
 ; PRIOR FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/085,579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: US 60/113,621
 ; PRIOR FILING DATE: 1998-12-23
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 24
 ; LENGTH: 206
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: IL-17C-His tag
 US-09-854-280-24

Query Match 17.3%; Score 170.5; DB 10; Length 206;
 Best Local Similarity 29.8%; Pred. No. 7.8e-09;
 Matches 53; Conservative 17; Mismatches 71; Indels 37; Gaps 7;
 QY 31 HTYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 73
 DB 27 HPHSHGTPTCHYSHMPSCPSKGDTSSELLRWSTVPPVPLEPARNHPESCRASE 81
 QY 74 CRASEDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDRGN 122

Db 82 PSATGCPVLRPEEVLADTHORSISPMWRYVDTEDEYRPOKLAFAECLRGCIDARTGR 141
OY 123 HMDPRGNSSELYNNQVYFRPCHGKNG---THKGYCLERLTVRSIACVCPRVWG 177
Db 142 ETAAL-NSVALLQSLVLRRRRPSRDSGLPTGCAFHTEFTLHVPGCTVLPFRSNG 198

RESULT 13
US-09-854-208-24
Sequence 24, Application US/09854208
Patent No. US20020106743A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Guiney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: P1381-R1
CURRENT APPLICATION NUMBER: US/09/854,208
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US/09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/113,621
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 24
LENGTH: 206
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Artificial sequence
LOCATION: 1-206
OTHER INFORMATION: IL-17C-His tag
US-09-854-208-24

Query Match 17.3%; Score 170.5; DB 10; Length 206;
Best Local Similarity 29.8%; Pred. No. 7.8e-09;
Matches 53; Conservative 17; Mismatches 71; Indels 37; Gaps 7;

OY 31 HYSHPSCPSKSGQDTSEEL-----LW-STVP---VPLEPARNRHPS 73
Db 27 HPHSGTPIGYS-----AEELPLGQAPPHLLARGAKMGQALPVALVSSLEAASHRGHNR 81
OY 74 CRASEDGPL-----NSRAISPMWRYELDRDLNRLPQDLYHARCLCPHCVSLQTS 122
Db 82 PSATGCPVLRPEEVLADTHORSISPMWRYVDTEDEYRPOKLAFAECLRGCIDARTGR 141
OY 123 HMDPRGNSSELYNNQVYFRPCHGKNG---THKGYCLERLTVRSIACVCPRVWG 177
Db 142 ETAAL-NSVALLQSLVLRRRRPSRDSGLPTGCAFHTEFTLHVPGCTVLPFRSNG 198

RESULT 14
US-09-874-503-4
Sequence 4, Application US/09874503
Patent No. US20020177188A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hymowitz, Sarah G.
APPLICANT: Tumas, Daniel

APPLICANT: Starovasanik, Melissa A.
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Vansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
TITLE OF INVENTION: P1381R1C1P3(US)
FILE REFERENCE: P1381R1C1P3(US)
CURRENT APPLICATION NUMBER: US/09/874,503
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/244,072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/213,807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/138,387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: US 60/134,287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/131,022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: US 60/130,232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/113,621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/644,848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/380,142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/380,138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US PCT/US00/15364
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/US00/04341
PRIOR FILING DATE: 2000-02-18

1	PRIOR APPLICATION NUMBER: 60/191007
2	PRIOR FILING DATE: 2000-03-21
3	PRIOR APPLICATION NUMBER: 60/213807
4	PRIOR FILING DATE: 2000-06-22
5	PRIOR APPLICATION NUMBER: 60/242837
6	PRIOR FILING DATE: 2000-10-24
7	PRIOR APPLICATION NUMBER: 60/244072
8	PRIOR FILING DATE: 2000-10-26
9	PRIOR APPLICATION NUMBER: 60/253646
10	PRIOR FILING DATE: 2000-11-28
11	PRIOR APPLICATION NUMBER: 09/311832
12	PRIOR FILING DATE: 1999-05-14
13	PRIOR APPLICATION NUMBER: 09/380138
14	PRIOR FILING DATE: 1999-08-25
15	PRIOR APPLICATION NUMBER: 09/380142
16	PRIOR FILING DATE: 1999-08-25
17	PRIOR APPLICATION NUMBER: 09/644848
18	PRIOR FILING DATE: 2000-08-22
19	PRIOR APPLICATION NUMBER: 09/747259
20	PRIOR FILING DATE: 2000-12-20
21	PRIOR APPLICATION NUMBER: 09/916744
22	PRIOR FILING DATE: 2001-03-22
23	PRIOR APPLICATION NUMBER: 09/854208
24	PRIOR FILING DATE: 2001-05-10
25	PRIOR APPLICATION NUMBER: 09/854280
26	PRIOR FILING DATE: 2001-05-10
27	PRIOR APPLICATION NUMBER: 09/874503
28	PRIOR FILING DATE: 2001-06-05
29	PRIOR APPLICATION NUMBER: 09/908827
30	PRIOR FILING DATE: 2001-07-18
31	PRIOR APPLICATION NUMBER: 09/918585
32	PRIOR FILING DATE: 2001-07-30
33	PRIOR APPLICATION NUMBER: 09/929404
34	PRIOR FILING DATE: 2001-08-13
35	PRIOR APPLICATION NUMBER: 09/931836
36	PRIOR FILING DATE: 2001-08-16
37	PRIOR APPLICATION NUMBER: PCT/US99/05028
38	PRIOR FILING DATE: 1999-03-08
39	PRIOR APPLICATION NUMBER: PCT/US99/10733
40	PRIOR FILING DATE: 1999-05-14
41	PRIOR APPLICATION NUMBER: PCT/US99/31274
42	PRIOR FILING DATE: 1999-12-30
43	PRIOR APPLICATION NUMBER: PCT/US00/04341
44	PRIOR FILING DATE: 2000-02-18
45	PRIOR APPLICATION NUMBER: PCT/US00/05601
46	PRIOR FILING DATE: 2001-03-01
47	PRIOR APPLICATION NUMBER: PCT/US00/05841
48	PRIOR FILING DATE: 2000-03-02
49	PRIOR APPLICATION NUMBER: PCT/US00/07532
50	PRIOR FILING DATE: 2000-03-21
51	PRIOR APPLICATION NUMBER: PCT/US00/15264
52	PRIOR FILING DATE: 2000-06-02
53	PRIOR APPLICATION NUMBER: PCT/US00/23328
54	PRIOR FILING DATE: 2000-08-24
55	PRIOR APPLICATION NUMBER: PCT/US00/30873
56	PRIOR FILING DATE: 2000-11-10
57	PRIOR APPLICATION NUMBER: PCT/US00/32678
58	PRIOR FILING DATE: 2000-12-01
59	PRIOR APPLICATION NUMBER: PCT/US00/34956
60	PRIOR FILING DATE: 2000-12-20
61	PRIOR APPLICATION NUMBER: PCT/US01/06522
62	PRIOR FILING DATE: 2001-02-28
63	PRIOR APPLICATION NUMBER: PCT/US01/17800
64	PRIOR FILING DATE: 2001-06-01
65	PRIOR APPLICATION NUMBER: PCT/US01/19699
66	PRIOR FILING DATE: 2001-06-20
67	PRIOR APPLICATION NUMBER: PCT/US01/21066
68	PRIOR FILING DATE: 2001-06-29
69	PRIOR APPLICATION NUMBER: PCT/US01/21733
70	PRIOR FILING DATE: 2001-07-09
71	NUMBER OF SEQ ID NOS: 39
72	SEQ ID NO 4
73	LENGTH: 197

TYPE: PRT
ORGANISM: Homo Sapien
us-10-000-157-4

Query Match 16.8%; Score 165.5; DB 9; Length 197;
Best Local Similarity 29.7%; Pred. No. 2.2e-08;
Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;

```

OY 31 HTYSHMPSCCPKSGQDTSEEL-----LRW-STVP--VPLEPARPNRHPES 73
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 27 HPHSHGTPHCYS-----AELPLGQAPPHLIARGAKWGQALPVALVSSLEASHRGHRER 81
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 74 CRASEDDGPL-----NSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLOTGS 122
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 82 PSATTCQCVLKPPEVLEADTHQRSISPWRYVDDEDREYPOKLAFAECLCRGCIIDARTGR 141
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 123 HMDPRGNSELLYHNOTVYFRRPCHGEGK---THKGYCLERRLRYSLACVCYRPR 174
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 142 ETAL-NSVRLQSLVLRPRPCSRDGSGLPTPGAFAFHTEFIHVPVGCCTCVLPR 195
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

Search completed: February 26, 2003, 09:34:08
Job time : 15 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:30:41 ; Search time 46 Seconds
(Without alignments)
369.909 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985
Sequence: 1 MRRPRRGEDSSLSIFLQV.....ERLLRVSLACVPRVWG 177

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	10.9	162	T32515	hypothetical prote
2	93.5	9.5	151	B45351	Immediate-early pr
3	91	9.2	150	T149623	cytotoxic T-lympho
4	88.5	9.0	422	A60503	sperm-binding glyco
5	86	8.7	147	JC4628	cytotoxic T-lympho
6	83	8.4	1323	T178557	N-methyl-D-asparta
7	81.5	8.3	467	A47388	serine/threonine p
8	78.5	8.0	206	T25139	hypothetical prote
9	78	7.9	358	JC00805	hydrogenase (EC 1.
10	77.5	7.9	961	JC00805	thrombospondin 4 p
11	77	7.8	263	TSHD4	hypothetical prote
12	77	7.8	344	T11776	N-methyl-D-asparta
13	76.5	7.7	1323	S27224	hypothetical prote
14	75.5	7.7	445	G85064	hypothetical prote
15	75.5	7.7	898	T14764	SH2-containing ino
16	75.5	7.7	1189	JC6118	gastric mucin MUC5
17	74.5	7.6	850	S56015	DNA topoisomerase
18	74.5	7.6	892	T06818	telomerase catalyt
19	74.5	7.6	1132	T03844	adenosine deaminas
20	74.5	7.6	1175	J01978	structural polypro
21	74.5	7.6	1254	J01978	gastric mucin MUC5
22	74.5	7.6	1373	J05095	DNA (cytosine-5)-
23	74.5	7.6	1612	JC5210	hypothetical prote
24	74	7.5	237	AJ0672	ADAM 6 protein pre
25	73.5	7.5	735	T148101	collagen alpha 1(X
26	73	7.4	482	B31795	GPI protein - mous
27	72.5	7.4	1840	T30250	insulin-like growt
28	72.5	7.4	240	A39842	hypothetical prote
29	72.5	7.4	294	T34537	hypothetical prote

30	72.5	7.4	419	2	T19871	hypothetical prote
31	72.5	7.4	602	2	H70796	hypothetical prote
32	72.5	7.4	1188	2	JC4889	phosphatidylinosit
33	72.5	7.4	1254	1	J01979	structural polypro
34	72.5	7.4	3744	2	S46715	hypothetical prote
35	72	7.3	216	2	T30657	hypothetical prote
36	72	7.3	238	2	T48605	insulin-like growt
37	72	7.3	360	1	S11968	hydrogenase (EC 1.
38	72	7.3	391	2	JC6193	tumor suppressor p
39	72	7.3	1348	2	S27812	probable epidermal
40	72	7.3	1348	2	A43917	hypothetical prote
41	71.5	7.3	166	2	C72734	hypothetical prote
42	71.5	7.3	650	2	AB2004	hypothetical prote
43	71.5	7.3	2319	2	A47004	coagulation factor
44	71	7.2	488	2	S13423	stromelysin 3 (EC
45	71	7.2	530	2	T30505	hypothetical prote

ALIGNMENTS

RESULT 1

T32515
hypothetical protein C44B12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T32515

R:Fin-William, A.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C44B12.

A:Reference number: 221183

A:Accession: T32515

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-162 <FIN>

A:Cross-references: EMBL:AF036692; PIDN:AA88329.1; GSPDB:GND00022; CESP:C44B12.6

A:Gene: CESP:C44B12.6

A:Map position: 4

A:Introns: 41/3; 95/3; 115/1

Query Match 10.9%; Score 107; DB 2; Length 162;

Best Local Similarity 26.2%; Pred. No. 0.011;

Matches 34; Conservative 23; Mismatches 39; Indels 34; Gaps 6;

QY 43 KGDTSELLRWSTVPVPLEPARPNRHRPESCRASEGCLMSRAISPRYELDRDLNRLP 102

Db 57 KSRDCSEPSIDKSEVL-----DQPLSERSTCYHHILNVDKRRIP 98

QY 103 QDLYHARCLCPHCVSLOTG-SHMDPRGNSSELLYHQTFYRRPCHGEQTHKGYCLERRL 161

Db 99 AAISEVSCSPH-VKVGHGIIHCEP-----MMYNKRWVLFDDSC--DK-----YVERV 143

QY 162 YRVSLACV 171

Db 144 QKVALACV 153

RESULT 2

B45351

Immediate-early protein 2 - saintmeline herpesvirus 1 (strain 11)

N:Alternate names: hypothetical protein ORF13

C:Species: saintmeline herpesvirus 1

A:Note: host saintmeline herpesvirus (common squirrel monkey)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C:Accession: B45351; D36807

R:Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.

Virology 179, 189-200, 1990

A:Title: Gene expression in cells infected with gammaherpesvirus saintmeline

A:Reference number: A45351; MUID:91021021; PMID:1699352

A:Accession: B45351

A:Molecule type: mRNA

RESULT 4
A60503

[illegible]

RESULT 6

178557 N-methyl-D-aspartate receptor chain NMDAR2D-2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
 C:Accession: 178557, 158158; D45219
 R:Monyer, H.; Burnashev, N.; Laurie, D.J.; Sakmann, B.; Seeburg, P.H.
 Neuron 12, 539-540, 1994
 A:Title: Developmental and regional expression in the rat brain and functional properties
 A:Reference number: 158158; PMID:94206533; PMID:7512349
 A:Accession: 178557
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1333 <RES>
 A:Cross-references: GB:L31612; NID:9469068; PIDN:AAC37647.1; PID:9469069
 A:Accession: 158158
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-66, 'V', 68-1323 <RE2>
 A:Cross-references: GB:L31611; NID:9469066; PIDN:AAC37646.1; PID:9469067
 R:Shi, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa
 J. Biol. Chem. 268, 2836-2843, 1993
 A:Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor
 A:Reference number: A45219; PMID:93155102; PMID:8428958
 A:Accession: D45219
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1265-1323 <ISH>
 A:Experimental source: brain
 A:Note: sequence extracted from NCBI backbone (NCBI:124265)
 C:Superfamily: N-methyl-D-aspartate receptor 2D: glutamate receptor homology
 F:451-879/Domain: glutamate receptor homology <GRH>

Query Match 8.4%; Score 83; DB 2; Length 1323;

Best Local Similarity 26.7%; Pred. No. 15;
 Matches 35; Conservative 7; Mismatches 39; Indels 50; Gaps 7;

QY 54 MSTVPPLEPAR--PNHPESCRASEDPGL-----NSRALSPRYELDRDLRLRP 103

DB 1202 WAGP-PPRRARCCGPRRPHRRASHRAAAPHNNHRRAGGDFPPPTSRSL 1260

QY 104 DL-----YHARCLCPHCV---SLQTGSHMDPRGNSSELLYHQTVEYRR 143

DB 1261 DSSCPRAAPTRRLTGPSRRAR-RCPHAAHWGPRPLTASHRRRG----- 1304

QY 144 PCGEGKTHKG 154

DB 1305 ---GDLGTRRG 1312.5

RESULT 7

A47388 serine/threonine protein kinase - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A47388
 R:Petrijotis, C.; Makris, A.; Bear, S.E.; Tschilis, P.N.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2251-2255, 1993
 A:Title: Tumor progression locus 2 (Tpl-2) encodes a protein kinase involved in the prog
 A:Reference number: A47388; PMID:93211939; PMID:768151
 A:Accession: A47388
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-467 <PAT>
 A:Cross-references: GB:M94454; NID:9207082; PIDN:AAA42185.1; PID:9207083
 A:Experimental source: liver
 A:Note: sequence extracted from NCBI backbone (NCBIN:128133, NCBI:128134)
 C:Superfamily: protein kinase homology
 F:136-388/Domain: protein kinase homology <KIN>

Query Match 8.3%; Score 81.5; DB 2; Length 467;
 Best Local Similarity 30.3%; Pred. No. 7;
 Matches 33; Conservative 8; Mismatches 37; Indels 31; Gaps 5;

QY 40 CPKGCQ--DTSEELRMSTVPPLEPAR-----PNHPESCRASEDP 81

DB 50 CPUSNOKHSESELRL-SCGEVPLSSVRGTVEDLLAFANHISNTKHFRCRPOESGI 108

QY 82 LNSRAISP--WRVELDRDLNRLPDOLYHARCLCPHCVSLQTGSHMDRG 128

DB 109 LLNMVISPONGROYDSDVLLVPMKLYR-----SIGSGVPRG 147

RESULT 8

T25139 hypothetical protein T22H6.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T25139
 R:McMurray, A.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: 219986
 A:Accession: T25139
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-206 <WIL>
 A:Cross-references: EMBL:250797; PIDN:CA90671.1; GSPDB:GN00028; CESP:T22H6.1
 A:Experimental source: clone T22H6
 C:Genetics:
 A:Gene: CESP:T22H6.1
 A:Map position: X
 A:Intons: 19/2; 80/3; 128/3; 162/3

Query Match 8.0%; Score 78.5; DB 2; Length 206;

Best Local Similarity 20.0%; Pred. No. 5.8;
 Matches 33; Conservative 21; Mismatches 46; Indels 65; Gaps 6;

QY 34 SHWPSCPS-----KGDTSEELRMSTVPPLEPARPNHPESCRA-----S 77

DB 63 SHSPSPSPSQALLRLQKGLKHGEQITKSS-----GKCNKKLDTIS 106

QY 78 EDGPLNSRAISPWRVELDRDLNRLPDOLYHARCLCPHCVSLQTGSHMDPRGNSSELL- 133

DB 107 AETPLDRALCKFEYLVNVPKRLPALTEVKSC-----PPNSKLVGKR 153

QY 134 -----YHQTVEYRRPCGEGKTHKGCLERLYSLACVY 171

DB 154 FEECHLRQYRVLMWDSCN-----TFREVERIALACIPV 189

RESULT 9

J00805 hydrogenase (EC 1.18.99.1) small chain precursor - Azotobacter vinelandii
 N:Alternate names: hydrogenlyase; [NiFe]hydrogenase
 C:Species: Azotobacter vinelandii
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
 C:Accession: J00805
 R:Monon, A.L.; Stults, L.W.; Robson, R.L.; Mortenson, L.E.
 Gene 96, 67-74, 1990
 A:Title: Cloning, sequencing and characterization of the [NiFe]hydrogenase-encodi
 A:Reference number: J00805; PMID:91092503; PMID:2265761
 A:Accession: J00805
 A:Molecule type: DNA
 A:Residues: 1-358 <MCN>
 A:Cross-references: GB:M33152; NID:9142310; PIDN:AAA82505.1; PID:9142311
 A:Experimental source: strain OP
 A:Note: part of this sequence, including the amino end of the mature protein, was
 C:Genetics:
 A:Gene: hoxK
 C:Complex: heterodimer: large and small chain
 C:Function:
 A:Pathway: hydrogen metabolism
 A:Note: contains iron-sulfur and nickel
 C:Superfamily: hydrogenase (NiFe) small chain
 C:Keywords: 3Fe-4S; 4Fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein;
 F:1-45/Domain: signal sequence #status predicted <SIG>

F:46-358/Product: hydrotgenase small chain #status experimental <MAY>
 F:62,65,160,194/Binding site: 4fe-4S cluster (Cys) (covalent) #status predicted
 F:232,233,260,266/Binding site: 4fe-4S cluster (His, Cys, Cys) (covalent) (type N3)
 F:275,294,297/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 7.9% Score 78; DB 1; Length 358;
 Best Local Similarity 21.9% Pred. No. 11;
 Matches 37; Conservative 19; Mismatches 35; Indels 78; Gaps 11;

QY 36 WSCSKGQDTSEELRWSTVPVPLEPARPNRHPSCRASDGLNSRAISPMRYELD 95
 DB 157 WSCSKA-----SMGCV-----QAAPN-----PTQAVPIHKVITD 185
 QY 96 RLNLRLPOLYLHARCLCPHCVSLQTS-----SHMDPRGNSELLY-----HNOQTF 140
 DB 186 KPIYKVPVPG-----CPPIAEVMTGVITMLTFGKLELDRCGRPMFYGORIHDKC-- 235
 QY 141 YRRPCH-----GKNGTHKGYCLERLRYVSL-----ACVCVR 172
 DB 236 YRRP-HRDAGQFVHMDEGARRKGYC---LYKVGCKGPTSYNACSTVR 279

RESULT 10

TSHUP4
 thrombospondin 4 precursor - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999

C:Accession: A55710; S36069

R:Lawley, J.; McHenry, K.; Duquette, M.; Derick, L.

J. Biol. Chem. 270, 2809-2814, 1995

A:Title: Characterization of human thrombospondin-4.

A:Reference number: A55710; MUID:95153552; PMID:7852353

A:Accession: A55710

A:Molecule type: mRNA

A:Residues: 1-961 <LAW>

A:Cross-references: EMBL:Z19585; NID:9311625; PIDN:CAA79635.1; PID:9311626

A:Note: authors translated the codon GTG for residue 616 as Ser

C:Genetics:

A:Gene: GDB:THBS4

A:Cross-references: GDB:463011; OMIM:600715

A:Map position: 1q21-1q23

C:Complex: homotrimer, disulfide linked

C:Function: participates in cell migration and adhesion, and in platelet aggregation

A:Superfamily: thrombospondin 3; EGF homology

C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; cell ad

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-961/Product: thrombospondin 4 #status predicted <MAY>

F:290-324/Domain: EGF homology <EGF>

F:330-362/Domain: EGF homology <EGF>

F:562-564/Region: cell attachment (R-G-D) motif

F:303/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:343/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

F:612,941/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.9% Score 77.5; DB 1; Length 961;
 Best Local Similarity 27.3% Pred. No. 34;
 Matches 38; Conservative 13; Mismatches 47; Indels 41; Gaps 8;

QY 7 LGEDSLISFLQYVAVLAWMGTHYTHSHMPCPSKGDTSSELLWSTV--PVPLLP 64
 DB 234 LGVKKDLRQVKTSTFL-----RNTIAECQACGLKFKQSTP-----STVADAPAPAP 283
 QY 65 ARPKRHES-----CRASED-----GLNSRAISPMRYE-----LDRDLNLRLPOLYL 106
 DB 284 TRPRRCDNSNCFRGVQCTDSRDGFQCGP-----CPGTYGNGITCIDVD-----ECKY 332
 QY 107 HARCLCPHCVSLQTSAMD 125
 DB 333 HPCYRGVHINLSPEGRCD 351

RESULT 11

T48742
 hypothetical protein 8D4.160 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
 C:Accession: T48742
 R:Schultz, U.; Algn, V.; Hohlisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyaka
 submitted to the Protein Sequence Database, April 2000

A:Reference number: 224541
 A:Accession: T48742
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-263 <SCH>
 A:Cross-references: EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.160
 A:Experimental source: cosmid contig 8D4; strain 74

C:Genetics:
 A:Gene: NCSP:8D4.160
 A:Map position: 2
 A:Inserts: 32/3; 76/1; 133/1
 C:Superfamily: Neurospora crassa hypothetical protein 8D4.160

Query Match 7.8% Score 77; DB 2; Length 263;
 Best Local Similarity 25.4% Pred. No. 10;
 Matches 34; Conservative 11; Mismatches 45; Indels 44; Gaps 8;

QY 36 WSCCKSKGQDTSE--ELRW--STVPVPLEPARPN-RHPSCRASE----- 78
 DB 43 WSSSLPVGKSKKATSRVWGASVEVPKAKIRARLTNDHCRPPMYTLRRDRMEAG 102
 QY 79 -----DGPL-----NSRAISPMRYE-----LDRDLNLRLPOL-----YARCLCPH----- 114
 DB 103 GSGWRPMDGFLPQCGRRHALYVWENSPSYDRSNANAOVLGALKRRARCCPQQLSSL 162
 QY 115 --CVSLQTSAMD 125
 DB 163 DGLCVRCYTGROTD 176

RESULT 12

S11776
 hydrotgenase (EC 1.18.99.1) (uptake) small chain precursor - Azotobacter chroococcum

C:Species: Azotobacter chroococcum

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000

C:Accession: S11776

R:Forst, C.M.; Garg, N.; Garg, R.P.; Tidellius, K.H.; Yates, M.G.; Arp, D.J.; Seefeld

Mol. Microbiol. 4, 999-1008, 1990

A:Title: The identification, characterization, sequencing and mutagenesis of the ge

A:Reference number: S11776; MUID:91014699; PMID:2215219

A:Accession: S11776

A:Molecule type: DNA

A:Residues: 1-344 <FOR>

A:Cross-references: EMBL:X52961; NID:938713; PIDN:CAA73133.1; PID:938714

A:Experimental source: strain MC01

C:Genetics:

A:Gene: hups

C:Complex: heterodimer; large and small chain

C:Function:

A:Pathway: hydrogen metabolism

A:Note: contains iron-sulfur and nickel

C:Superfamily: hydrotgenase (Nlfe) small chain

C:Keywords: 3fe-4S; 4fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein;

F:1-34/Domain: signal sequence #status predicted <SIG>

F:35-344/Product: hydrotgenase (uptake) small chain #status predicted <MAY>

F:51,54,146,180/Binding site: 4fe-4S cluster (Cys) (covalent) #status predicted

F:218,221,246,252/Binding site: 4fe-4S cluster (His, Ser, Cys, Cys) (covalent) (typ

F:261,280,283/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 7.8% Score 77; DB 1; Length 344;
 Best Local Similarity 21.3% Pred. No. 13;
 Matches 36; Conservative 21; Mismatches 34; Indels 78; Gaps 11;

QY 36 WSCCKSKGQDTSEELRWSTVPVPLEPARPNRHPSCRASEDGLNSRAISPMRYELD 95
 DB 143 WSCSKA-----SMGCV-----QAAPN-----PTQAVPIHKVITD 171

QY 96 RDLNRLPDLYHARCLSPHCVSLQTS-----SHMDRGNSELLY-----HNQTFV 140
 DB 172 KPMIKVPG-----CPRIAEVMGVITMYLTFGLPDLRGGRRKMYGGQRINRKS--- 221
 QY 141 YRRPCH-----GEGTKHGVCLEERLYRVSL-----ACVCVR 172
 DB 222 YRRP-HEFAGQFVEHMDGARGKGC-----LYKVGCKGPTSYNACSTVR 265

RESULT 13

S27224
 N-methyl-D-aspartate receptor epsilon-4 chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
 C:Accession: S27224
 R:Ikeda, K.; Nagasawa, M.; Mori, H.; Arai, K.; Sakimura, K.; Inoue, Y.; M
 FEBS Lett. 313, 34-38, 1992
 A:Title: Cloning and expression of the epsilon-4 subunit of the NMDA receptor channel.
 A:Reference number: S27224; MUID:93050214; PMID:1385220
 A:Accession: S27224
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1323 <IKE>
 A:Cross-references: EMBL:DJ2822
 C:Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
 C:Keywords: transmembrane protein
 F:451-879/Domain: glutamate receptor homology <GRH>

Query Match 7.8%; Score 76.5; DB 2; Length 1323;
 Best Local Similarity 25.5%; Pred. No. 59;
 Matches 35; Conservative 6; Mismatches 41; Indels 55; Gaps 7;

QY 54 WSTVPV-----PLEPAR-----PNRNPESCRASEDRL-----NSRAISPMRYELDRD 97
 DB 1195 WAPRRPAAAPRRARRARCCSRPRNRPRASHRAAARNHNRRAAGMDLPPRAP 1254
 QY 98 LNRLEPDL-----YHARCLSPHCV-----SLQTSMDRGNSELLYHNO 137
 DB 1255 TSSLEDLSCPRAPRTLRTPSRNAR-RCPNAAHWGPRPLTASHRRRG----- 1304
 QY 138 TVFYRRPCHGEKTHKG 154
 DB 1305 -----GDLGTRRG 1312

RESULT 14

G85064
 hypothetical protein AT4G05150 (imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: G85064
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: G85064
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-446 <STO>
 A:Cross-references: GB:NC_001268; NID:97267274; PIDN:CAB81057.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4G05150
 A:Map position: 4

Query Match 7.7%; Score 75.5; DB 2; Length 446;
 Best Local Similarity 22.7%; Pred. No. 24;
 Matches 30; Conservative 21; Mismatches 44; Indels 37; Gaps 6;

QY 44 GQDSEELLRMTVPVPP-----LEPAR-----NRHPSCRASEDGLNSRAISPMRY 92
 DB 249 GTSASAVMTRISTELPPPVIRKPSPEPVSTPKSNPQEQVMOQSNLPLVNSQ---WQY 304

QY 93 E-----LDRDLNRLPDLYHARCLSPHCVSLQTSMDRGNSELL----- 132
 DB 305 ARPGQOQVHYQGHTTHQSP--WYVPGSYRGNHNMVQGGNHNMVQRYVQMPQQLQ 362
 QY 133 LYHNOTVIFYRRP 144
 DB 363 QYHNVPMGYHNP 374

RESULT 15

T14764
 hypothetical protein DKFZp434H204.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T14764
 R:Wambolt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, August 1999
 A:Reference number: T18181
 A:Accession: T14764
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-898 <NAN>
 A:Cross-references: EMBL:AL110226
 A:Experimental source: adult testis; clone DKFZp434H204
 C:Genetics:
 A:Note: DKFZp434H204.1

Query Match 7.7%; Score 75.5; DB 2; Length 898;
 Best Local Similarity 24.4%; Pred. No. 49;
 Matches 31; Conservative 9; Mismatches 48; Indels 39; Gaps 6;

QY 34 SHMPSCPKSGQDSEELLRMTVPVPP--EPARNHPSCRASEDGLNSRAISPMR 91
 DB 739 SSMRECSACGGGEGQRLV--TCPEGLCEALRN-----TTRCNHPCIQWVGPRV 790
 QY 92 YELDRDLNRLPDLYHARCLP-----HCYSLQTSMDRGNSELLYHNOTIFY 141
 DB 791 -----GQCSAPCGGGVQRRLYKCVNTQTGL--PEEDSDCGHNAWPRS 831
 QY 142 RRPCHGE 148
 DB 832 SRPCGTE 838

Search completed: February 26, 2003, 09:33:28
 Job time: 49 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:08:55 ; Search time 13 Seconds
(without alignments)
564.716 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985
Sequence: 1 MRRPRPLGDSLSLFLVY.....ERRLYRSLACVPRVPMG 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	985	100.0	177	117E_HUMAN	Q9H293 homo sapien
2	165.5	16.8	197	117C_HUMAN	Q9P0M4 homo sapien
3	125.5	12.7	180	117B_HUMAN	Q9UHT5 homo sapien
4	123.5	12.5	180	117E_MOUSE	Q9GHT6 mus musculu
5	122	12.4	153	117E_HUMAN	Q9GPT4 homo sapien
6	116.5	11.8	178	117E_MOUSE	Q9GHT6 mesocricetu
7	105.5	10.7	155	117E_HUMAN	Q16552 homo sapien
8	93.5	9.5	151	117E_MOUSE	Q16552 herpessvirus
9	91	9.2	150	117E_MOUSE	Q16552 mus musculu
10	90.5	9.2	151	117E_MOUSE	Q16552 mus musculu
11	88.5	9.0	151	117E_MOUSE	Q16552 mus musculu
12	88.5	9.0	151	117E_MOUSE	Q16552 mus musculu
13	83	8.4	133	117E_MOUSE	Q16552 mus musculu
14	81.5	8.3	133	117E_MOUSE	Q16552 mus musculu
15	78	7.9	133	117E_MOUSE	Q16552 mus musculu
16	77.5	7.9	133	117E_MOUSE	Q16552 mus musculu
17	77.5	7.9	133	117E_MOUSE	Q16552 mus musculu
18	77.5	7.9	133	117E_MOUSE	Q16552 mus musculu
19	77.5	7.9	133	117E_MOUSE	Q16552 mus musculu
20	77.5	7.9	133	117E_MOUSE	Q16552 mus musculu
21	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
22	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
23	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
24	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
25	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
26	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
27	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
28	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
29	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
30	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
31	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
32	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu
33	76.5	7.8	133	117E_MOUSE	Q16552 mus musculu

34	72.5	7.4	1254	1	POL5_EEYVM	P36331 venezuelan
35	72.5	7.4	3695	1	LMAS_HUMAN	O15230 homo sapien
36	72.5	7.4	3744	1	YHP9_YEAST	P38811 saccharomyc
37	72.5	7.3	391	1	IBP6_MOUSE	P47880 mus musculu
38	72.5	7.3	391	1	P53_RABIT	Q95330 oryctolagus
39	71.5	7.3	2319	1	F8A2_MOUSE	Q06194 mus musculu
40	71	7.2	488	1	MM11_HUMAN	P24347 homo sapien
41	71	7.2	1333	1	SOS1_HUMAN	Q07889 homo sapien
42	71	7.2	2208	1	POLN_MANCV	Q05901 manchester
43	70.5	7.2	914	1	PERT_MOUSE	P35419 mus musculu
44	70	7.1	198	1	XAL_XENLA	P23507 xenopus lae
45	70	7.1	479	1	FLRD_SALTI	Q824c5 salmoneilla

ALIGNMENTS

RESULT 1
ID 117E_HUMAN STANDARD: PRT: 177 AA.

AC Q9H293;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-17E precursor (IL-17E).

DE IL17E.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID:9606;

RN (1)

RP MEDLINE:21125711; PubMed:11058597;

RA Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,

RA Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;

RT "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog

RT IL-17Rhl.";

RL J. Biol. Chem. 276:1660-1664(2001).

CC -1- FUNCTION: Induces activation of NF-kappaB and stimulates

CC -1- production of the proinflammatory chemokine IL-8;

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed at low levels in several tissues,

CC including brain, kidney, lung, prostate, testis, spinal cord,

CC adrenal gland, and trachea.

CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@sib-sib.ch).

CC EMBL: AF305200; AAC0848.1;

CC Gene: HGNC:13765; IL17E.

CC MIM: 605658;

CC Cytokine; Glycoprotein; Signal.

CC SIGNAL

CC CHAIN

CC DISULFID

CC DISULFID

CC CARBOHYD

CC SEQUENCE

CC 177 AA; 20330 MW; 52D89571DCD59871 CRC64;

CC Query Match

CC Best Local Similarity 100.0%; Score 985; DB 1; Length 177;

CC Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 MRRPRPLGDSLSLFLVYVFLAVWVGTHRTYSHMPCCPKSGQDTSELLRLMSTVPP 60

CC 1 MRRPRPLGDSLSLFLVYVFLAVWVGTHRTYSHMPCCPKSGQDTSELLRLMSTVPP 60

QY 61 PLEPARPNHPCSCRASEDGCLNSRAISPMRYELDRDLNLPDLYHARCICPHCVSLQT 120
 |||
 DB 61 PLEPARPNHPCSCRASEDGCLNSRAISPMRYELDRDLNLPDLYHARCICPHCVSLQT 120
 |||
 QY 121 GSHMDRGNSSELLYHNOTVFRPCHGKGTAKGKCYCLERLYVSLACVCPRRWG 177
 |||
 DB 121 GSHMDRGNSSELLYHNOTVFRPCHGKGTAKGKCYCLERLYVSLACVCPRRWG 177
 |||
 RESULT 2
 ID 117C_HUMAN STANDARD: PRT: 197 AA.
 AC 09H04: 09H04: 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17C precursor (IL-17C) (Cytokine CX2).
 GN IL17C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20105548; PubMed-10639155;
 RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
 RA Gurney A.L., Wood W.I.;
 RA "Cloning and characterization of IL-17B and IL-17C, two new members
 RT of the IL-17 cytokine family";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP Zhang W., He L., Wan T., Yuan Z., Cao X.;
 RA "Novel human cytokine CX2 with homology to IL-17";
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha
 CC and IL-1beta from the monocytic cell line THP-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF152099; AAF28105.1;
 DR EMBL: AF142410; AAG27921.1;
 DR GenBank: HGNC:5983; IL17C.
 DR MIM: 604628;
 DR Cytokine; Signal.
 FT CHAIN 1 18
 FT SIGNAL 1 18
 FT CHAIN 19 197
 FT DISULFID 129 189
 FT DISULFID 134 191
 FT CONFLICT 50 50
 FT SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;
 Query Match 16.8%; Score 165.5; DB 1; Length 197;
 Best Local Similarity 29.7%; Pred. NO. 8.8e-09;
 Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;
 QY 31 HTYSHMPCSCPKQDTSEEL-----LRW-STVP-----VPLEPARPNHPC 73
 |||
 DB 27 HPHSHGPHPCYS-----AELPLQADPPHLLARAKAGQALPVALLVSLLEAASHRGHER 81
 |||
 QY 74 CRASEDGPL-----NSRAISPMRYELDRDLNLPDLYHARCICPHCVSLQTS 122
 |||
 DB 82 PSATTCQCVLAPREVLADTHQHSISPMRYELDRDLNLPDLYHARCICPHCVSLQTS 141
 |||
 QY 123 HMDPRGNSSELLYHNOTVFRPCHGKGTAKGKCYCLERLYVSLACVCPRR 174
 |||

DB 142 ETAL-NSVRLLOSLVLRPCSCRGSGLPFGARAFHTEFHVVGCVLP 195
 |||
 RESULT 3
 ID 117B_HUMAN STANDARD: PRT: 180 AA.
 AC 09H05;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYT07)
 DE (Neuronal Interleukin-17 related factor) (Interleukin-20).
 GN IL17B OR ZCYT07 OR NIRE OR IL20.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RP Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
 RA Martinez T., Hoffman R., O'Hara P.;
 RA Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-20317118; PubMed-10749887;
 RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
 RA Barber M.C., Wang W., Mathen K., Hodge V., Fisher C.L., Olsen H.,
 RA Ruben S.M., Knayazov I., Cho Y.H., Kao V., Wilkinson K.A.,
 RA Darrell J.A., Ebner R.;
 RA "A novel cytokine receptor-ligand pair. Identification, molecular
 RT characterization, and in vivo immunomodulatory activity";
 RT J. Biol. Chem. 275:19167-19176(2000).
 RL [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-20105548; PubMed-10639155;
 RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
 RA Gurney A.L., Wood W.I.;
 RA "Cloning and characterization of IL-17B and IL-17C, two new members
 RT of the IL-17 cytokine family";
 RT Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
 RL [4]
 RN SEQUENCE FROM N.A.
 RP Moore E.E., Presnell S., Garrigues U., Guilbot A., Leclercq E.,
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
 RA "Identification of a novel IL-17 related factor: demonstration of
 RT neuronal expression and evaluation as a candidate for the chromosome
 RT 5q-linked form of Charcot-Marie-Tooth disease";
 RT Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RN SEQUENCE FROM N.A.
 RP Zhang W., Wang J., Cao X.;
 RA "Novel cytokine homology with Interleukin-17";
 RT Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RN SEQUENCE FROM N.A.
 RP Rieder M.J., Garrington D.P., Chung M.-W., Lee K.L., Peel C.L., Yi Q.,
 RA Nickerson D.A.;
 RA Submitted (Jun-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha
 CC and IL-1beta from the monocytic cell line THP-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed in adult pancreas, small intestine,
 CC stomach, spinal cord and testis. Less pronounced expression in
 CC prostate, colon mucosal lining, and ovary.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@sb-sib.ch).

CC EMBL: AF184969; AAF01318.1; -
 CC EMBL: AF212311; AAF78775.1; -
 DR EMBL: AF152098; AAF28104.1; -
 DR EMBL: AF216727; AAG44136.1; -
 DR EMBL: AF10385; AAG39637.1; -
 DR EMBL: AF386077; AAK60336.1; -
 DR GeneB; HGNC:5982; IL17B.
 DR MIM: 604627; -
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 180
 FT DISULFID 121 176
 FT DISULFID 126 178
 FT CARBOHYD 75 75
 FT SEQUENCE 180 AA; 20437 MW; 11B0B01446D0B14A CRC64;
 SO
 Query Match 12.7%; Score 125.5; DB 1; Length 180;
 Best Local Similarity 33.3%; Pred. No. 4.9e-05;
 Matches 30; Conservative 16; Mismatches 39; Indels 5; Gaps 3;

OY 83 NSRAISPMRYELDRDLNLPOLYHARCLCPHCYSLQTSMDPRGNSLLYHNOVTFYR 142
 ID 117B_MOUSE STANDARD; PRT; 180 AA.
 AC Q9QXT6; Q9QXT4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 precursor (IL-17) (Cytokine-like protein ZCYT07)
 DE Interleukin-17 related factor (Cytokine CX1).
 DE (Neuronal Interleukin-17 related factor) (Cytokine CX1).
 GN IL17 OR ZCYT07 OR N1RF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
 RA Martinez T., Hoffman R., O'Hara P.,
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguern E.,
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.,
 RT "Identification of a novel IL-17 related factor: demonstration of
 RT neuronal expression and evaluation as a candidate for the chromosome
 RT 5q-linked form of Charcot-Marie-Tooth disease."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BALB/C;
 RC Zhang W., Cao X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-Embryo;
 RC MEDLINE=21085660; PubMed=11217851;
 RX Kanai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirm L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinaci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Grynchich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RL
 RN
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha
 CC and IL-1beta from the monocytic cell line THP-1 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sb-sib.ch).

CC EMBL: AF184970; AAF01319.1; -
 CC EMBL: AF218726; AAG44135.1; -
 CC EMBL: AF250308; AAK37427.1; -
 CC EMBL: AK003506; BAB28226.1; -
 CC EMBL: BC002271; AAH02271.1; -
 CC MGD; MGI:1928397; IL17b
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 180
 FT DISULFID 121 176
 FT DISULFID 126 178
 FT CARBOHYD 75 75
 FT CARBOHYD 75 75
 FT CONFLICT 33 33
 FT CONFLICT 34 34
 FT CONFLICT 65 65
 FT CONFLICT 76 76
 FT CONFLICT 76 76
 FT SEQUENCE 180 AA; 20309 MW; E26FAC72001997C5 CRC64;
 SO
 Query Match 12.5%; Score 123.5; DB 1; Length 180;
 Best Local Similarity 32.2%; Pred. No. 7.6e-05;
 Matches 29; Conservative 17; Mismatches 39; Indels 5; Gaps 3;

OY 83 NSRAISPMRYELDRDLNLPOLYHARCLCPHCYSLQTSMDPRGNSLLYHNOVTFYR 142
 ID 117F_HUMAN STANDARD; PRT; 153 AA.
 AC Q96PD4; Q9NUE6; Q96P18;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 precursor (IL-17) (Interleukin-24) (Cytokine ML-1).
 DE IL17 OR IL24.
 GN Homo sapiens (Human).
 OS

ID	IL17_HUMAN	STANDARD:	PRT:	155 AA.			
Db	8	SIL16LASEAANKIKKVGHTFFQKRESP	-----	-PYPGSGMKLDIGI 51			
Qy	67	PNRHPESRSESDPPLNSRAISPMRYELDLRLPDLGYHARCPCRCVSLDTGSHMP		126			
Db	52	IN-----ENQVRASMSNISERSSTPMNVYTVTMDPDPSEVQAOCCRNIGICNAO-----		101			
Qy	127	RGNSESLLYHN-----QTFYRPRCHGSKGNHKGCCLERLRYRSLACVCFP		173			
Db	102	GKEDIAMNSVPIQOETLVARRK---HGGCSVSQLEKVL--VTGCTCTGTF		147			
RESULT 6							
ID	117B_MESAU	STANDARD:	PRT:	178 AA.			
IL17B_MESAU							
Qy	15-JUN-2002 (Rel. 41, Created)						
DR	15-JUN-2002 (Rel. 41, Last sequence update)						
DT	15-JUN-2002 (Rel. 41, Last annotation update)						
DE	Interleukin-17 precursor (IL-17b) (Neutroal Interleukin-17 related factor) (Fragment).						
GN	IL17B OR N1RF						
OC	Mesocricetus auratus (Golden hamster).						
OC	Makroryta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;						
OC	Mesocricetus.						
OX	NCBI_TaxID=10036;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguern E.,						
RA	Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;						
RT	Identification of a novel IL-17 related factor: demonstration of						
RT	neutroal expression and evaluation for a candidate for the chromosome						
RL	5q-linked form of Charcot-Marie-Tooth disease."						
RL	Submitted (DEC-1999) to the EMBL/Genbank/DBD databases						
CC	1- FUNCTION: Stimulates the release of tumor necrosis factor alpha						
CC	and IL-1beta from the monocytic cell line THP-1 (By similarity).						
CC	1- SUBCELLULAR LOCATION: Secreted.						
CC	1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.						
CC	1- This SWISS-PROT entry is copyright. It is produced through a collaboration						
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation						
CC	at the European Bioinformatics Institute. There are no restrictions on its						
CC	use by non-profit institutions as long as its content is in no way						
CC	modified and this statement is not removed. Usage by and for commercial						
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/						
CC	or send an email to license@isb-sib.ch).						
CC	DR EMBL; AF218725; AAC4134.1;						
CC	Cyclokin; Glycoprotein; Signal.						
FT	SIGNAL 1 22						
FT	CHAIN 23 >178						
FT	CARBOHYD 75 75						
FT	DISULFID 121 176						
FT	DISULFID 126 178						
FT	NON_TER 178 178						
FT	SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;						
Query Match							
Best Local Similarity 32.6%; Pred. No. 0.00034;							
Matches 29; Conservative 14; Mismatches 41; Indels 5; Gaps 3							
Qy	83	NSRAISPMRYELDLRLNLPDLGYHARCPCRCVSLDTGSHMPRGNSESLLYHNQTFYR		142			
Db	94	NKRSLSPMGYSINHPSRIPADLPARCLGCGVNPFT--MQEDRSNVSVPVPSQVYVR		151			
Qy	143	RPCHGSKGNHKGCCLERLRYR-VSLACV		170			
Db	152	RLC--PPRRPGRPCRHRYMETIANGCIC		178			
RESULT 7							
IL17_HUMAN							
STANDARD:							
PRT: 155 AA.							
IL17_HUMAN							

AC 016552;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 precursor (IL-17) (IL-17A) (Cytotoxic T lymphocyte-
 associated antigen 8) (CTLA-8).
 GN IL17 OR IL17A OR CTLA8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96281911; PubMed-8676080;
 RA Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Alt-Yahia S.,
 RA Mat C., Pin J.-J., Garonne P., Garcia E., Saeland S., Blanchard D.,
 RA Galliard C., Das Mahapatra B., Rouvier E., Golstein P., Banchereau J.,
 RA Lebecque S.;
 RT "T cell interleukin-17 induces stromal cells to produce
 RT proinflammatory and hematopoietic cytokines.";
 RL J. Exp. Med. 183:2593-2603(1996).
 RN
 RP SEQUENCE FROM N.A.
 RX TISSUE-T-cell;
 RX MEDLINE-96094436; PubMed-7499628;
 RA Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M.,
 RA Spiggs M.K., Armitage R.J.;
 RT "Human IL-17: a novel cytokine derived from T cells.";
 RL J. Immunol. 155:5483-5486(1995).
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND
 CC HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE
 CC INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.
 CC -1- PIM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC -1- DATABASE: NAME-RED Systems' cytokine mitr-reviews: IL17;
 CC WWW="http://www.indsystems.com/asp/g_silebuilder.aspbodyId=211".
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Z58820; CA91233.1;
 DR EMBL: U32659; AAC50341.1;
 DR GeneW; HGNC:5981; IL17.
 DR MIM: 603149;
 DR Cytokine; Glycoprotein; T-cell; Antigen; Signal.
 KM CHAIN 1 23 POTENTIAL.
 FT SIGNAL 1 23 INTERLEUKIN-17.
 FT DISULFID 24 155 BY SIMILARITY.
 FT DISULFID 94 144 BY SIMILARITY.
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 155 AA; 17504 MW; 2BCA93CB2F488601 CRC64;
 Query Match 10.7%; Score 105.5; DB 1; Length 155;
 Best Local Similarity 27.1%; Pred. No. 0.0033;
 Matches 45; Conservative 27; Mismatches 73; Indels 21; Gaps 8;
 QY 11 SLSLSFLQVAVFLAMVNGTHTYSHWPCSCPSKGDTSBELRMSTVPP-PLPAPRPNR 69
 DB 6 TSLVSLLL-LLSLEAIVAGITIPRNPCCPNSEDKNFR-----TVAVNLIHNRNMT 58
 QY 70 HPESRASEDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLOPHCVSLQTSCHMDPRGN 129
 DB 59 NKR--RSSD---YNNRSTSPMNLHNRDEPERPYIWEAK--CRHLGICINADGNVDYHNN 111
 QY 130 SELLYHNQTVFYRRPCHGEGKTHKGYCLERLLRYSLACVAPRPV 175

DB 112 SVPIQCEIIVLRREPPIH-----CPNSFLREKIL--VSVGCTCVPPIV 151
 RESULT 8
 ID VGI3_HSVSA STANDARD; PRT; 151 AA.
 AC P24916;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Immediate early gene 13 protein precursor.
 GN 13 OR KCLF2.
 OS Herpesvirus saimiri (strain 11).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OC NCBI_TaxID=10383;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90163221; PubMed-2154888;
 RA Albrecht J.-C., Fleckenstein B.;
 RT "Structural organization of the conserved gene block of Herpesvirus
 RT saimiri coding for DNA polymerase, glycoprotein B, and major DNA
 RT binding protein.";
 RL Virology 174:533-542(1990).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92333688; PubMed-1321287;
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Blesinger B.,
 RA Newman C.W., Wiltmann S., Craxton M.A., Coleman H., Fleckenstein B.,
 RA Honess R.;
 RT "Primary structure of the herpesvirus saimiri genome.";
 RL J. Virol. 66:5047-5058(1992).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91021021; PubMed-1699352;
 RA Nicholas J., Smith E.P., Coles L., Honess R.;
 RT "Gene expression in cells infected with gammaherpesvirus saimiri:
 RT properties of transcripts from two immediate-early genes.";
 RL Virology 179:189-200(1990).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X64346; CA45636.1;
 DR EMBL: M31122; AAA46169.1;
 DR EMBL: M60286; AAA46156.1;
 DR PIR: D36807; D36807.
 DR PIR: B45351; B45351.
 DR Cytokine; Early protein; Signal.
 KM CHAIN 1 22 POTENTIAL.
 FT SIGNAL 1 22 IMMEDIATE EARLY GENE 13 PROTEIN.
 FT CHAIN 23 151 BY SIMILARITY.
 FT DISULFID 90 140 BY SIMILARITY.
 FT DISULFID 95 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 151 AA; 17180 MW; 53BEDDE4206C432 CRC64;
 Query Match 9.5%; Score 93.5; DB 1; Length 151;
 Best Local Similarity 23.0%; Pred. No. 0.044; Indels 41; Gaps 8;
 Matches 40; Conservative 28; Mismatches 65;
 QY 11 SLSLSFLQVAVFLAMVNGTHTYSHWPCSCPSKGDTSBEL-----RSTVVPPLPRA 65
 DB 6 TSLVSLLL--LSDICVKSSEITSQTPRCLANNSPRASVWVTLSTIRNMT----- 54

OY 66 RRRHRESCRAEDGDPINRAISPMREYELDRDLNRLPODLYHARCICPHCVSLQTSMD 125
 DB 55 -----SSKRAD--YYRSTSPWTLHRNEDODRYPVIMEKCYLCGVAND----- 99
 OY 126 PRGNSELHNOCTVFYRRCPC---HGEKGTGKCYCLERLYRVSACVCPRV 175
 DB 100 --GNVD--YHMSVPIQOELLYVRKGHCPCPNSEFLEKML--VTGCTCTVTPIV 147

RESULT 9

IL17_RAT STANDARD: PRT; 150 AA.

AC 061453:
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).
 GN IL17 OR CTLA8.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93294300; PubMed=8390535;
 RA Ruvier E., Luciani M.F., Mattei M.-G., Denizot F., Golstein P.; CTLA-8, cloned from an activated T cell, bearing Au-rich messenger RNA instability sequences, and homologous to a herpesvirus salmirel gene.
 RT J. Immunol. 150:5445-5456(1993).
 RL [2]
 RN ORGANISM IDENTIFICATION.
 RP MEDLINE=96194901; PubMed=8654948;
 RX Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.; *Complete nucleotide sequence of the mouse CTLA8 gene.*
 RT Gene 168:223-225(1996).
 RL [3]
 RN SEQUENCE FROM N.A. AND ORGANISM IDENTIFICATION.
 RX MEDLINE=97031826; PubMed=8877732;
 RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A., Wagner J.L., Hannum C.H., Zlotnik A.; *Mouse IL-17, a cytokine preferentially expressed by alpha beta TCR + CD4-CD8-T cells.*
 RT J. Interferon Cytokine Res. 16:611-617(1996).
 RL J. Interferon Cytokine Res. 16:611-617(1996).
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE FROM MOUSE BUT, ON THE BASIS OF SUBSEQUENT WORK (REF.2 AND REF.3), HAS BEEN SHOWN TO BE OF RAT ORIGIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: L13839; AAA37490.1; -
 KM Cytokine; Glycoprotein; T-cell; Antigen; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 150
 FT DISULFID 89 139
 FT DISULFID 94 141
 FT CARBOHYD 63 63
 FT CONFLICT 46 46
 FT SEQUENCE 150 AA: 16876 MW: 16876 MW: EF13F33EDFD689F CRC64;

Query Match 9.2%; Score 91; DB 1; Length 150;
 Best Local Similarity 29.7%; Pred. No. 0.075;
 Matches 30; Conservative 17; Mismatches 44; Indels 10; Gaps 5;

OY 73 SCRASEDGPUN--SRAISPMREYELDRDLNRLPODLYHARCICPHCVSLQTSMDPRGNS 130
 DB 50 SSKASSRRSPDYLNRSPTWTLHRNEDPDPRYPVIMEACRHCRCVNAE--GKLDHMS 107
 OY 131 ELLYHNOCTVFYRRCPCGCKGTGKCYCLERLYRVSACV 171
 DB 108 VLIQOELLYVRKGHCPCPNSEFLEKML--VTGCTCTVTPIV 142

RESULT 10

IL17_MOUSE STANDARD: PRT; 158 AA.

AC 062386; Q60971;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).
 GN IL17 OR CTLA8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BA16/C; TISSUE=Thymocytes;
 RX MEDLINE=97031826; PubMed=8877732;
 RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A., Wagner J.L., Hannum C.H., Zlotnik A.; *Mouse IL-17, a cytokine preferentially expressed by alpha beta TCR + CD4-CD8-T cells.*
 RT J. Interferon Cytokine Res. 16:611-617(1996).
 RL J. Interferon Cytokine Res. 16:611-617(1996).
 RN SEQUENCE OF 12-158 FROM N.A.
 RC STRAIN=129/SV; TISSUE=T-cell;
 RX MEDLINE=96194901; PubMed=8654948;
 RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.; *Complete nucleotide sequence of the mouse CTLA8 gene.*
 RT Gene 168:223-225(1996).
 RL J. Interferon Cytokine Res. 16:611-617(1996).
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U43088; AAB05232.1; -
 DR EMBL: U35108; AAA3253.1; -
 DR GMD: MG1:107364; 1117
 KM Cytokine; Glycoprotein; T-cell; Antigen; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 158
 FT DISULFID 97 147
 FT DISULFID 102 149
 FT CARBOHYD 71 71
 FT SEQUENCE 158 AA: 17490 MW: 3505C143435F453 CRC64;

Query Match 9.2%; Score 91; DB 1; Length 158;
 Best Local Similarity 23.5%; Pred. No. 0.079;
 Matches 39; Conservative 29; Mismatches 72; Indels 26; Gaps 7;

OY 11 SSLISLQVAVFLAMVGTHTYSHMPCSCPSKSG-----ODTSEELRMSTVVPPLPEPA 65
 DB 6 ASSSVLMLLLSLAATVKKAAIIPSSCAPTEAKDFLOWKVKVFNLSIGA-KVSSR 64
 OY 66 RPNRHPSCRASSEDGPLNSRAISFWRELDRLRQDLYHACLCPCHCISLQTSMD 125
 DB 65 RPSDY-----LN-RSTSPWTLHRNEDPRYPVINEACORHORCVNAE--GKLD 110
 OY 126 PRGSELLHNQTVFYRPRCHGKTHKCYCLERLYVSLACV 171
 DB 111 HHMNSVLIOEILVLRKP-----ESCPFTFVEKML-VGVGCTCV 150

RESULT 11
 ID VGI3_HSVSC STANDARD: PRT: 151 AA.

AC 040633: 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Immediate early gene 13 protein precursor.
 CN 13.
 OS Herpesvirus saimiri (subgroup C / strain 488).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=10384;
 RN MEDLINE FROM N.A.
 RA MEDLINE=98037620; PubMed=9371569;
 RA Knäuper A., Hüller C., Thurn M., Wiltmann S., Hofmann H.,
 RA Fleckenstein B., Fleckenstein H.,
 RT "The superantigen-homologous viral immediate-early gene iel4/vsag 1a
 RT herpesvirus saimiri-transformed human T cells."
 RL J. Virol. 71:9124-9133(1997).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: Y13183; CAA73627.1;
 CC DR Cytokine; Early protein; Signal.
 CC FT SIGNAL 1 22; POTENTIAL.
 CC FT CHAIN 23 151 IMMEDIATE EARLY GENE 13 PROTEIN.
 CC FT DISULFID 90 140 BY SIMILARITY.
 CC FT DISULFID 95 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 36 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 9.2%; Score 90.5; DB 1; Length 151;
 Best Local Similarity 23.0%; Pred. No. 0.084;

Matches 40; Conservative 27; Mismatches 66; Indels 41; Gaps 8;

OY 11 SSLISLQVAVFLAMVGTHTYSHMPCSCPSKSGODTSEELL-----RMSVVPPLPEPA 65
 DB 6 TSVLULLL--LSIDCIYSEITSQTPRLAANNSFPSPVVTLSIRMNT----- 54
 OY 66 RPNRHPSCRASSEDGPLNSRAISFWRELDRLRQDLYHACLCPCHCISLQTSMD 125
 DB 55 -----SSKRASD--YVNRSTSPWTLHRNEDPRYPVINEACORHORCVNAE----- 99
 OY 126 PRGSELLHNQTVFYRPRCHGKTHKCYCLERLYVSLACVCPRPV 175
 DB 100 --GNVD--YHNSVPIQOELLVVRKGHNPCPSFRLKML--VTGVCCTVPTIV 147

RESULT 12
 ID ZP3_MESAU STANDARD: PRT: 422 AA.
 AC P23491:
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Zona pellucida sperm-binding protein 3 precursor (Zona pellucida
 DE glycoprotein zp3) (sperm receptor) (Zona pellucida protein C).
 GN zp3.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN MEDLINE FROM N.A.
 RA MEDLINE=91078540; PubMed=2257975;
 RA Kinsch R.A., Ruiz-Seller B., Massarman P.M.;
 RT "Genomic organization and polypeptide primary structure of zona
 RT pellucida glycoprotein zp3, the hamster sperm receptor."
 RL Dev. Biol. 142:414-421(1990).
 CC -1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR
 CC SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE
 CC SPECIES-SPECIFICITY OF THE INSEMINATION.
 CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN
 CC WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Extracellular
 CC matrix.
 CC -1- TISSUE SPECIFICITY: OOCYTES.
 CC -1- DEVELOPMENTAL STAGE: GROWING OOCYTES.
 CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.
 CC -1- SIMILARITY: CONTAINS 1 ZP DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: M63629; AAA37079.1;
 CC DR InterPro: IPR001507; Endoglin/CD105.
 CC DR Pfam: PF00100; zona_pellucida; 1.
 CC DR PRINTS: PRO0023; ZPPELLUCIDA.
 CC DR SMART: SM00241; zp: 1.
 CC DR PROSITE: PS00682; ZP_DOMAIN; 1.
 CC KW Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane;
 CC KW Extracellular matrix.
 CC FT SIGNAL 1 22 POTENTIAL.
 CC FT CHAIN 23 422 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3.
 CC FT DOMAIN 23 386 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 387 407 POTENTIAL.
 CC FT DOMAIN 408 422 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 45 306 ZP.
 CC FT DOMAIN 119 158 PRO-RICH.
 CC FT DOMAIN 208 257 PRO-RICH.
 CC FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SEQUENCE 422 AA; 45827 MW; D0F95BE7FF8E7E01 CRC64;

Query Match 9.0%; Score 88.5; DB 1; Length 422;
 Best Local Similarity 28.8%; Pred. No. 0.4;

Matches 42; Conservative 19; Mismatches 46; Indels 39; Gaps 9;

OY 7 LGEDS--SLISLQVAVFLAMVGTHTYSHMPCSCPSKSGODTSEELLRMSTV-----P 58
 DB 73 LGSNCRPLVAVATDVVRKQAL--HE-----CSNRVQVT-EDALVYSTLLHQRP 121
 OY 59 VPLEPAPRNH--PESCRASEDGPLNSRAISFWRELDRLN-----RLPQDLYH 107

DB 122 VPELSLRTVRADVPTECRPRGQNVSSHAIRPTWPFSTVSSEKLVSLRLMEENM 181
 QY 108 ARCLCP--HC-----VSIQTGSHM 124
 DB 182 TEKLSPSTSLGGEVAYLQAEVQTSHTL 207

RESULT 13
 MME4_RAT STANDARD: PRT: 1323 AA.
 ID MME4_RAT 062645; 063381; 063382; 063729; 063730.
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Glutamate [NMDA] receptor subunit epsilon 4 precursor (N-methyl
 D-aspartate receptor subtype 2D) (NR2D) (NMDAR2D).
 GN GRIN2D.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1] SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 1265-1356 FROM N.A.
 RP (ISOFORM 2).
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;
 RX MEDLINE=93155102; PubMed=8428958;
 RA Ishii T., Moriyoshi K., Sugihara H., Sakurada K., Kadotani H.,
 Yohoi M., Nakazawa G., Shigemoto R., Mizuno N., Nakanishi S.,
 RT "Molecular characterization of the family of the N-methyl-D-aspartate
 receptor subunits.", J. Biol. Chem. 268:2836-2843(1993).
 RL [2] SEQUENCE FROM N.A. (ISOFORM 2).
 RN TISSUE-Brain;
 RP MEDLINE=94206533; PubMed=7512349;
 RX Monyer H., Burnashev N., Laurie D.J., Sakmann B., Seeburg P.H.,
 RT "Developmental and regional expression in the rat brain and functional
 properties of four NMDA receptors.", Neuron 12:529-540(1994).
 RL [3] SEQUENCE FROM N.A. (ISOFORM 2).
 RN STRAIN-Sprague-Dawley; TISSUE-Brain;
 RP Boulder J., Pecht G.,
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS
 WITH HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT
 SENSITIVITY TO MAGNESIUM, MEDIATED BY GLYCINE.
 CC - SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZETA SUBUNIT.
 CC - SUPPLEMENTARY LOCATIONS: Integral membrane protein.
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 AND 2 (SHOWN HERE); MAY BE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC - TISSUE SPECIFICITY: EXPRESSED IN BRAIN, MAINLY IN THE SUBOPTICAL
 REGION.
 CC - DEVELOPMENTAL STAGE: Already detected in embryonic stages, peaks
 at postnatal day 7, and decreases thereafter to adult levels.
 CC - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D13213; BAA02500.1; -
 DR EMBL: D13214; BAA02501.1; -
 DR EMBL: L31611; AAC37646.1; -
 DR EMBL: L31612; AAC37647.1; -
 DR EMBL: U08260; AAA17833.1; -
 DR HSSP: P19491; IGR2.
 DR InterPro: IPR001320; Ion_glu_receptor.

DR InterPro: IPR001508; NMDA_receptor.
 DR InterPro: IPR001311; SBP/glu_receptor.
 DR Pfam: PR00060; Iig_chan. 1.
 DR PRINTS: PR00177; NMDARECEPTOR.
 DR ProDom: PD000500; Ion_glu_receptor; 1.
 DR SMART: SM00079; pape; 1.
 DR Receptor: Signal; Transmembrane; Postsynaptic membrane; Calcium;
 KW Glycoprotein; Ionic channel; Magnesium; Alternative splicing.
 FT CHAIN 1 27
 FT SIGNAL 1 27
 FT 28 1323
 FT DOMAIN 28 580
 FT TRANSMEM 581 601
 FT DOMAIN 602 623
 FT TRANSMEM 624 644
 FT DOMAIN 645 653
 FT TRANSMEM 654 674
 FT DOMAIN 675 841
 FT TRANSMEM 842 862
 FT DOMAIN 863 1323
 FT DOMAIN 278 283
 FT DOMAIN 905 913
 FT DOMAIN 1030 1035
 FT DOMAIN 1197 1201
 FT SITE 639 639
 FT CARBOHYD 89 89
 FT CARBOHYD 349 349
 FT CARBOHYD 363 363
 FT CARBOHYD 464 464
 FT CARBOHYD 566 566
 FT VARSPLIC 1265 1323
 FT 25 25
 FT CONFLICT 47 47
 FT CONFLICT 67 67
 FT CONFLICT 94 94
 FT CONFLICT 305 305
 FT CONFLICT 635 635
 FT CONFLICT 974 974
 FT CONFLICT 1253 1253
 FT CONFLICT 1266 1267
 FT SEQUENCE 1323 AA; 143100 MW; 40F7D60192579564 CRC64;
 Query Match 8.4%; Score 83; DB 1; Length 1323;
 Best local similarity 26.7%; Pred. No. 4.6; Mismatches 39; Indels 50; Gaps 7;
 Matches 35; Conservative 7; Mismatches 39; Indels 50; Gaps 7;
 QY 54 WSTVVPVPLEPAR---PNRPFESCRASEDGL-----NSRAISPMRYELDRDLNRLPQ 103
 DB 1202 WAAGP-PPRRRRACGCPRRPHRRASHRAAPAAHHHRRRAAGGDFPPAPTSSTLE 1260
 QY 104 DL-----YARCLCPHCV---SLQTGSHMDPRGNSSELYHNOYFYRR 143
 DB 1261 DLSSCPRAATRRLTGSGRIAR-RCPIAAHMGRLPLTASRRHRG----- 1304
 QY 144 PCHEKGTGKG 154
 DB 1305 ---GDLGTRRG 1312

RESULT 14
 M3K8_RAT STANDARD: PRT: 467 AA.
 ID M3K8_RAT 063562;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase kinase 8 (EC 2.7.1.-) (Tumor
 progression locus 2) (TPL-2).

3 OYAAETAMMGSTHTYSHWSPCCPSKGGDTSEELLRWSTVVPPLLEPARPNRHRESCRASE 64

OY 79 DGPLNSRAISPMWRELDRLNRLPDLIYHARCCLPHCVSLQTSMDPRGNSSELYHNQT 138
 |||||||
 DB 63 DGPLNSRAISPMWRELDRLNRLPDLIYHARCCLPHCVSLQTSMDPRGNSSELYHNQT 122
 |||||||
 OY 139 VFYRPPCHGEKGTGKGYCLERLYRVSLACVCPVRPM 176
 |||||||
 DB 123 VFYRPPCHGEKGTGKGYCLERLYRVSLACVCPVRPM 160
 |||||||

RESULT 2

OYVNH8 PRELIMINARY: PRT: 169 AA.

AC OYVNH8: 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE IL25.

GN IL17E.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6;

RC MEDLINE=21629216; PubMed=11754819;

RA Fort M.M., Cheung J., Yen D., Li J., Zurawski S.M., Lo S., Menon S.,

RA Clifford T., Hunte B., Lesley R., Muchamuel T., Hurst S.D.,

RA Zurawski G., Leach M.W., Gorman D.M., Rennick D.M.;

RT "IL-25 induces IL-4, IL-5, and IL-13 and Th2-associated pathologies in

RT VIVO."

RL Immunity 15:985-995(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Hurst S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,

RA Kwan S., Menon S., Seymour B., Jackson C., Kung T., Brieland J.,

RA Zurawski S.M., Chapman R., Zurawski G., Coffman R.L.;

RT "New IL-17 family members promote Th1 or Th2 responses in the lung: in

RT vivo function of the novel cytokine IL-25."

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF458060; AAL57623.1; "

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21571724; PubMed=11714825;
 RA Pan G., French D., Mao W., Marucka M., Risse P., Lee J., Foster J.,
 RA Aggarwal S., Nicholas K., Guillet S., Schow P., Gurney A.L.;

RT "Forced Expression of Murine IL-17E Induces Growth Retardation,

RT Jaundice, a Th2-Biased Response, and Multicystic Inflammation in

RT Mice."

RL J. Immunol. 167:6559-6567(2001).

DR EMBL: AY034088; AAK59816.1; "

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

DR MCD: MGI:2155888; IL17E.

Query Match 66.2%; Score 652; DB 11; Length 153;
 Best Local Similarity 81.1%; Pred. No. 4,7e-62;
 Matches 116; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 34 SHMPCSPKSGQDTSEELRMSTVPPLEPARPNRHPESCRASEDGPLNSRAISPMWRE 93
 |||||||
 DB 10 SHMPCSPKSGQDTSEELRMSTVPPLEPARPNRHPESCRASEDGPLNSRAISPMWRE 69
 |||||||
 OY 94 LDRDLNRLPDLIYHARCCLPHCVSLQTSMDPRGNSSELYHNQTFYRPPCHGEKGTGK 153
 |||||||
 DB 70 LDRDLNRLPDLIYHARCCLPHCVSLQTSMDPRGNSSELYHNQTFYRPPCHGEKGTGK 129
 |||||||
 OY 154 GYCLERLYRVSLACVCPVRPM 176
 |||||||
 DB 130 GYCLERLYRVSLACVCPVRPM 152
 |||||||

RESULT 4

OYVNH8 PRELIMINARY: PRT: 202 AA.

AC OYVNH8: 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Interleukin 27 precursor (IL27 precursor).

GN IL27.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=ENTIRE BRAIN;

RA Haddi-Slimane R., Bobe P.;

RT "Interleukin 27 (IL27): a newly identified cytokine."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF078238; AAL86911.1; "

DR EMBL: AF479775; AAM12734.1; "

DR EMBL: AF479775; AAM12734.1; "

DR EMBL: AF479775; AAM12734.1; "

DR EMBL: AF479775; AAM12734.1; "

DR EMBL: AF479775; AAM12734.1; "

DR EMBL: AF479775; AAM12734.1; "

DR EMBL: AF479775; AAM12734.1; "

DR EMBL: AF479775; AAM12734.1; "

Query Match 12.8%; Score 126.5; DB 4; Length 202;
 Best Local Similarity 27.0%; Pred. No. 1.2e-05;
 Matches 44; Conservative 17; Mismatches 69; Indels 33; Gaps 6;

OY 36 WPCSPKSGQDTSEELRMSTVPPLEPARPNRHPESCRASEDGPLNSRAISPMWRE 72
 |||||||
 DB 14 WPCSPKSGQDTSEELRMSTVPPLEPARPNRHPESCRASEDGPLNSRAISPMWRE 73
 |||||||

1003

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE Hypothetical 55.5 kDa protein.
 OS Trypanosoma cruzi.
 CC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 NCBI_Taxid=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andersson B.
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF242860; AAF98145.1;
 KW Hypothetical protein.
 SQ SEQUENCE 499 AA; 55486 MW; 6727C831B8425296 CRC64;

Query Match 8.8%; Score 87; DB 5; Length 499;
 Best Local Similarity 28.3%; Pred. No. 0.56;
 Matches 32; Conservative 14; Mismatches 33; Indels 34; Gaps 6;

QY 37 PSCCPKSGDPT---SEELRMSTVPVPLEPAPRNHPESCR-----ASEDGPLN-----83
 DB 234 PSSPSDGTTRSMQKLRKQSIPIPARHGE-KREPETDRQHLLCGSETEFLNSGRHP 292
 QY 84 -----SAISPMRYELDRDLRLPODLYHARCICPHCVSLQTSMDPRGNSL 132
 DB 293 SOQSSRVLS-----SPSPNDVFHD-----TPIQSLHSGRGYSEI 329

RESULT 9

ID Q9BU21 PRELIMINARY; PRT; 405 AA.
 AC Q9BU21;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Similar to hypothetical protein FLJ10101.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC002945; AAH02945.1;
 KW Hypothetical protein.
 SQ SEQUENCE 405 AA; 44298 MW; 6C30D7F7B60DBE68 CRC64;

Query Match 8.4%; Score 83; DB 4; Length 405;
 Best Local Similarity 24.3%; Pred. No. 1.2;
 Matches 44; Conservative 10; Mismatches 51; Indels 76; Gaps 9;

QY 55 STVEVPLEPAPRNHPESCRASEDGPLNSRAI-----SPMYELDRDLRLPQ-----103
 DB 217 SVPPVPPE-ALP---PPACPSA---PAPRSIISRPPEWRLGALGRGQMPWGGG 269
 QY 104 -----DLYHARCICP-----113
 DB 270 RACHCLGNHLPYHRLCKCPAAVACASLEENGHWSPGMALVGLAOCPEPALOEGRG 329
 QY 114 HCVSLQTSMDPRGNSLHYNQTVFYRRPCHGKTHKGYCLERRLYRSLACVYRP 173
 DB 330 QLASARLGGHPPLG-----AEPVFLRDVTEAOGEPVR-VCLD-RLGRGLAVGALP 381

QY 174 R 174
 DB 382 R 382

RESULT 10
 Q9ME9 PRELIMINARY; PRT; 547 AA.
 ID Q9ME9
 AC Q9ME9;

DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE rRNA -glycosidase (EC 3.2.2.22).
 GN AAG.
 OS Abrus precatorius (indian licorice) (Crab's eye).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eufrosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 NCBI_Taxid=3816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20102702; PubMed-10636890;
 RX Liu C.L., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
 Lin J.Y.,

RT Primary Structure and Function Analysis of the Abrus precatorius
 RT Agglutinin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic
 RT alpha-Helix H Impairs Protein Synthesis Inhibitory Activity."
 RL J. Biol. Chem. 275:1897-1901(2000).
 CC - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC - SPECIFIC ADENOSINE ON THE 28S RNA.
 CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
 CC EMBL: AF190173; AAF28309.1;
 DR HSP; P1140; IABR.
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PRO0396; SHIGARICIN.
 DR SMART: SM00458; RICIN_2.
 DR PROSITE: PS00231; RICIN_B_LCTIN; 2.
 DR PROSITE: PS00275; SHIGA_RICIN; UNKNOWN_1.
 DR Hydrolase; Toxin.
 KW SEQUENCE 547 AA; 61248 MW; 355A325C2354A1BD CRC64;

Query Match 8.4%; Score 83; DB 10; Length 547;
 Best Local Similarity 22.3%; Pred. No. 1.7;
 Matches 25; Conservative 18; Mismatches 55; Indels 14; Gaps 3;

QY 1 MREPRLEDESSLSLFLQVAVFLAMVGHHTYSHWPSCEPSKQDPTSEELRMSTVPV 60
 DB 412 MRQGMRTGNDTS--PFTVSIAGFKLCMEAGNSMMDVLC-----DITKEQOMAVYPDG 464
 QY 61 PLEPAPRNHPESCRASEDGPL-----NSRAISPMRYELDRDLRLPQDL 105
 DB 465 SIRVQNTNNCLTCEHKGATVMMGCSNMAWSQRYFRKDGITLYNLYDM 516

RESULT 11

ID Q9VS89 PRELIMINARY; PRT; 1394 AA.
 AC Q9VS89;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE G67526 protein (Fragment).
 GN G67526.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BERKELEY;
 RC MEDLINE-20196006; PubMed-10731132;
 RX Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
 RA Van K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Liao X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mikhlin N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palzozo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sieden-Kiamos I., Stapleton M., Strong R., Sun E.,
 RA Splitter E., Spirdling A.C., Stappleton M., Venter E., Wang X.,
 RA Svitskas R., Tector C., Turner R., Venter E., Weissbach J.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Skupski M.P., Smith T.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03558; AAF50538.1; -.
 DR HSSP: P00736; IAPQ.
 DR Flybase: FBgn0035798; CG7526.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR003410; Hyalin.
 DR InterPro: IPR000436; Sush1_SCR_CCP.
 DR InterPro: IPR001491; Thrombomodulin.
 DR Pfam: PF00008; EGF_11.
 DR Pfam: PF00084; sush1_2.
 DR PRINTS: PR00907; THROMBOMODULN.
 DR SMART: SM00032; CCP_2.
 DR SMART: SM00179; EGF_CA_9.
 DR SMART: SM00001; ASX_HYDROXYL_5.
 DR PROSITE: PS00010; ASX_HYDROXYL_8.
 DR PROSITE: PS01186; EGF_2-9.
 DR PROSITE: PS01187; EGF_CA_10.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 KW NON_TER 1394 1394
 FT SEQUENCE 1394 AA; 152269 MW; CD29380E3162F68A CRC64;
 SQ
 Query Match 8.2%; Score 81; DB 5; Length 1394;
 Best Local Similarity 26.5%; Pred. No. 7.8;
 Matches 27; Conservative 8; Mismatches 41; Indels 26; Gaps 5;
 Oy 72 ESCRASEDGPLNSRAISPRYELDRDLNLPDLYHARCLCPHCVSLQTSHPDPRGNS 131
 Db 322 DCDTLENNQNL-----RTKCAHECDLPREGSY--RCVCKRGYGLSLSDQH----- 364
 Oy 132 LLYHNQTVFYRRPCHGKGTNR--GYCLERLLRYSLACVC 170
 Db 365 -----SCLVQESPCSTREKGVCKSPGTCLASE-DNYSFSCIC 400
 RESULT 12
 O9NKZ8 PRELIMINARY: PRT; 379 AA.
 AC O9NKZ8;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE HgtrpN3 protein (Fragment).
 GN HgtrpN3.
 OS Eptatretus burgeri (Inshore hagfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotretii; Myxiniiformes;
 OC Myxiniidae; Eptatretinae; Eptatretus.
 OX NCBI_TaxID=7764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20219325; PubMed-10754074;
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
 RT divergence of tissue-specific isofom genes in the early evolution of
 RT vertebrates";
 RL J. Mol. Evol. 50:302-311(2000).
 DR EMBL: AB033579; BAA95186.1; -.
 DR HSSP: P18031; 2HNO.
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR000387; Tyr_phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00102; Y_phosphatase_1.
 DR PRINTS: PR00700; PRTYPPHTASE.
 DR SMART: SM00194; PTPC_1.
 DR SMART: SM00012; PTPC_DSPC_1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolyase.
 FT NON_TER 1
 FT SEQUENCE 379 AA; 42672 MW; A2493B3FEF3D90174 CRC64;
 SQ
 Query Match 8.2%; Score 80.5; DB 13; Length 379;
 Best Local Similarity 28.0%; Pred. No. 2.1;
 Matches 33; Conservative 9; Mismatches 45; Indels 31; Gaps 6;
 Oy 22 AFLAMVGTHTYTHMPSCCKSGK---QDNSEELRW-----STVPVPLEP--- 64
 Db 166 SFLALIGGMHLS--ADACGEGYLDDEEDNMSPEWYFAFPSPSTPPPPPPPPPKR 223
 Oy 65 --ARPNRHP-----ESCRASEDGPLNS--RAISPRYELDRDLNLPDLYHARC 110
 Db 224 STERNGGPAAKSNVYEDLTQTELPNNRDELLSPRYERKLDGCGVDEAFGERG 281
 RESULT 13
 O9P914 PRELIMINARY: PRT; 358 AA.
 AC O9P914;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Nitrate reductase subunit 2 (EC 1.7.99.4).
 GN NARH.
 OS Haloarcula marismortui (Halo bacterium marismortui), and
 OS Haloarcula marismortui subsp. marismortui.
 OC Archaea; Euryarchaeota; Halo bacteriia; Halobacteriales;
 OC Halobacteriaceae; Haloarcula.
 OX NCBI_TaxID=2238, 122093;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-H.marismortui;
 RA Yoshimatsu K., Iwasaki T., Fujiwara T.;
 RT "Sequence and Electron Paramagnetic Resonance Analyses of the Archaea
 RT Nitrate Reductase NARH from the Denitrifying Halophilic Euryarchaeote
 RT Haloarcula marismortui.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-H.marismortui subsp. marismortui;
 RA Yoshimatsu K., Yamamoto A., Fujiwara T.;
 RT "Sequence analysis of the dissimilatory nitrate reductase from a
 RT denitrifying halophilic archaean, Haloarcula marismortui,";
 RL submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ429077; CAD22070.1; -.

